Bowman, A.
10/773678
Seq. 10 342

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 6, 2005, 09:58:01 ; Search time 1445 Seconds
(without alignments)
670.660 Million cell updates/sec

Title: US-10-773-678-342
Perfect score: 20
Sequence: 1 gactcttgcaggaagcggct 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 790860

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
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6: gb_pat:*
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9: gb_pr:*
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11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	14	70.0	20	6	AR120998	AR120998 Sequence
	2	14	70.0	20	6	BD272619	BD272619 Antisense
	3	14	70.0	20	6	AR531367	AR531367 Sequence
	4	13	65.0	19	4	DOGP45501	L24340 Dog (Clone:
	5	12.8	64.0	20	6	BD228539	BD228539 IL-17 hom
	6	12.8	64.0	20	6	AR359764	AR359764 Sequence
c	7	12.6	63.0	20	6	CQ798932	CQ798932 Sequence
	8	12.4	62.0	17	6	A89364	A89364 Sequence 15
	9	12.4	62.0	17	6	AX672730	AX672730 Sequence
	10	12.4	62.0	17	6	AX762313	AX762313 Sequence
	11	12.4	62.0	17	6	BD066877	BD066877 An antise
	12	12.4	62.0	18	6	AX117443	AX117443 Sequence
c	13	12.4	62.0	20	6	AR098941	AR098941 Sequence
c	14	12.4	62.0	20	6	AR164768	AR164768 Sequence
c	15	12.4	62.0	20	6	BD222879	BD222879 KVLQT1-QT
c	16	12.4	62.0	20	6	I79781	I79781 Sequence 77
c	17	12.4	62.0	20	6	AR218732	AR218732 Sequence
c	18	12.4	62.0	20	6	AR223147	AR223147 Sequence
c	19	12.4	62.0	20	6	AR229909	AR229909 Sequence
c	20	12.4	62.0	20	6	AR262165	AR262165 Sequence
c	21	12.4	62.0	20	6	AR344603	AR344603 Sequence
	22	12.2	61.0	17	6	CQ623374	CQ623374 Sequence
	23	12.2	61.0	17	6	AR464437	AR464437 Sequence
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	26	12	60.0	17	6	AX674695	AX674695 Sequence
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	31	11.8	59.0	17	6	BD259356	BD259356 Regulatio
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c	42	11.6	58.0	20	6	AR361458	AR361458 Sequence
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	44	11.6	58.0	20	6	AR361503	AR361503 Sequence
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c	98	11.2	56.0	18	6	BD244849	BD244849 Polynucle
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ALIGNMENTS

RESULT 1
AR120998
LOCUS AR120998 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 19 from patent US 6159694.
ACCESSION AR120998
VERSION AR120998.1 GI:14104574
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Karras,J.G.
TITLE Antisense modulation of stat3 expression
JOURNAL Patent: US 6159694-A 19 12-DEC-2000;
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"
/mol_type="unassigned DNA"
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Query Match 70.0%; Score 14; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.7e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 7 GACTCTTGCAGGAA 20

RESULT 2
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LOCUS BD272619 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Antisense oligonucleotide modulation of STAT3 expression.
ACCESSION BD272619
VERSION BD272619.1 GI:33082387
KEYWORDS JP 2002541784-A/19.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Karras,J.G.
TITLE Antisense oligonucleotide modulation of STAT3 expression
JOURNAL Patent: JP 2002541784-A 19 10-DEC-2002;
ISIS PHARMACEUTICALS INC
COMMENT OS Artificial Sequence
PN JP 2002541784-A/19
PD 10-DEC-2002
PF 06-APR-2000 JP 2000611544
PR 08-APR-1999 US 09/288461
PI JAMES G KARRAS
PC C12N15/09,A61K31/711,A61K48/00,A61P29/00,A61P29/00,A61P35/00,
PC A61P37/02,
PC A61P43/00,C12N5/06,C12Q1/02,C12N15/00,C12N5/00 CC Antisense
oligonucleotide
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 7 GACTCTTGCAGGAA 20

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AR531367
LOCUS AR531367 20 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 19 from patent US 6727064.
ACCESSION AR531367
VERSION AR531367.1 GI:53919806
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Karras,J.G.
TITLE Antisense oligonucleotide modulation of STAT3 expression
JOURNAL Patent: US 6727064-A 19 27-APR-2004;
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Best Local Similarity 100.0%; Pred. No. 9.7e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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||||||||||||||
Db 7 GACTCTTGCAGGAA 20

RESULT 4
DOGP45501
LOCUS DOGP45501 19 bp DNA linear MAM 22-JAN-1996
DEFINITION Dog (Clone: CXX.455) primer for STS 455, 5' end.
ACCESSION L24340
VERSION L24340.1 GI:402053
KEYWORDS PCR identification; PCR primer; STS.
SEGMENT 1 of 2
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 19)
AUTHORS Ostrander,E.A., Mapa,F.A., Yee,M. and Rine,J.
TITLE One hundred and one new simple sequence repeat-based markers for
the canine genome
JOURNAL Mamm. Genome 6 (3), 192-195 (1995)
MEDLINE 95268214
PUBMED 7749226
COMMENT Original source text: Canis familiaris (library: E. Ostrander, in
pBluescript+) adult spleen DNA.
Submitted by:
Fred Hutchinson Cancer Research Center
Transplantation Biology Dept
1124 Columbia; Mailstop M318
Seattle, WA 98104, USA
e-mail: EAOstrander@lbl.gov
PCR Buffer: PCR buffer (Perkin-Elmer/Cetus)
PCR Profile: Denaturation: 94 degrees C for 1.00 minute
Annealing: 55 or 59 degrees C for 0.45 minutes
Polymerization: 74 degrees C for 1.00 minutes

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            PCR Cycles:      33
            Final Extension:  74 degrees C for 5.00 minutes.
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  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 TCTTGCAGGAAGC 16
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Db          4 TCTTGCAGGAAGC 16


RESULT 5
BD228539
LOCUS       BD228539                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  IL-17 homologous polypeptide and its application to remedy.
ACCESSION   BD228539
VERSION     BD228539.1  GI:33038309
KEYWORDS    JP 2002515246-A/134.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Chen,J., Filvaroff,E., Goddard,A., Gurney,A.L., Li,H. and Wood,W.I.
  TITLE     IL-17 homologous polypeptide and its application to remedy
  JOURNAL   Patent: JP 2002515246-A 134 28-MAY-2002;
            GENENTECH INC
COMMENT     OS   Unidentified
            PN   JP 2002515246-A/134
            PD   28-MAY-2002
            PF   14-MAY-1999 JP 2000549734
            PR   15-MAY-1998 US    60/085579,23-DEC-1998 US    60/113621 PI
            JIAN CHEN,ELLEN FILVAROFF,AUDLEY GODDARD,AUSTIN L GURNEY, PI
            HANZHONG LI,
            PI   WILLIAM I WOOD
            PC   C12N15/09,A61K38/21,A61K45/00,A61P19/00,C07K14/52,C07K16/24,
            PC   C07K19/00,
            PC   C12N1/19,C12N1/21,C12N5/10,C12P21/02,C12P21/08,C12Q1/00 PC
            ,C12Q1/68,C12N15/00,
            PC   A61K37/66,C12N5/00
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            CC   Topology: Linear;
            CC   IL-17 homologous polypeptide and its application to remedy FH
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  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Db          1 TCTTCCAGGAAGCTGC 16


RESULT 6
AR359764
LOCUS       AR359764                  20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 134 from patent US 6593456.
ACCESSION   AR359764
VERSION     AR359764.1  GI:33766508
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Gatanaga,T. and Granger,G.A.
  TITLE     Tumor necrosis factor receptor releasing enzyme
  JOURNAL   Patent: US 6593456-A 134 15-JUL-2003;
FEATURES              Location/Qualifiers
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  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 TCTTGCAGGAAGCGGC 19
              ||||  ||||||||  ||
Db          1 TCTTCCAGGAAGCTGC 16


RESULT 7
CQ798932/c
LOCUS       CQ798932                  20 bp    DNA     linear   PAT 28-APR-2004
DEFINITION  Sequence 13 from Patent WO2004031412.
ACCESSION   CQ798932
VERSION     CQ798932.1  GI:46847945
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Nakamura,Y. and Katagiri,T.
  TITLE     Method for diagnosing pancreatic cancer
  JOURNAL   Patent: WO 2004031412-A 13 15-APR-2004;
            Oncotherapy Science, Inc. (JP); Japan as represented by the
            president of the university of Tokyo (JP)
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Db         20 AATCTCCCAGGAAGCTGCT 2


RESULT 8
A89364
LOCUS       A89364                    17 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 1512 from Patent WO9833904.
ACCESSION   A89364
VERSION     A89364.1  GI:6737934
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
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  AUTHORS   Brysch,W. and Schlingensiepen,K.
  TITLE     AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
  JOURNAL   Patent: WO 9833904-A 1512 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES             Location/Qualifiers
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ORIGIN

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Db          4 ACTCTTGCAGGTAG 17


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LOCUS       AX672730                  17 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 1175 from Patent WO03004526.
ACCESSION   AX672730
VERSION     AX672730.1  GI:29331078
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
  JOURNAL   Patent: WO 03004526-A 1175 16-JAN-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
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ORIGIN

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              | ||||||||||||
Db          3 TCCAGGAAGCGGCT 16


RESULT 10
AX762313
LOCUS       AX762313                  17 bp    DNA     linear   PAT 25-JUN-2003
DEFINITION  Sequence 5634 from Patent WO03040369.
ACCESSION   AX762313
VERSION     AX762313.1  GI:32256929
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
  JOURNAL   Patent: WO 03040369-A 5634 15-MAY-2003;
            Molecular Engines Laboratories (FR)
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Db          3 TCTTGCAGGAAGAG 16


RESULT 11
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LOCUS       BD066877                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  An antisense oligonucleotide preparation method.
ACCESSION   BD066877
VERSION     BD066877.1  GI:22612480
KEYWORDS    JP 2001511000-A/1512.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Schlingensiepen,K.H. and Brysch,W.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: JP 2001511000-A 1512 07-AUG-2001;
            BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT     OS   Unknown
            PN   JP 2001511000-A/1512
            PD   07-AUG-2001
            PF   30-JAN-1998 JP 1998532533
            PR   31-JAN-1997 EP   97101531.8
            PI   KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
            PC   C12N15/11,C07H21/04,A61K31/70
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  Query Match             62.0%;  Score 12.4;  DB 6;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 6e+05;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 ACTCTTGCAGGAAG 15
              |||||||||| ||
Db          4 ACTCTTGCAGGTAG 17


RESULT 12
AX117443
LOCUS       AX117443                  18 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 2566 from Patent WO0129262.
ACCESSION   AX117443
VERSION     AX117443.1  GI:14034394
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Picoult-Newburg,L. and Pohl,M.
  TITLE     Genotyping reagents, kits and methods of use thereof
  JOURNAL   Patent: WO 0129262-A 2566 26-APR-2001;
            Orchid BioSciences, Inc. (US)
FEATURES             Location/Qualifiers
```

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     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"
ORIGIN

  Query Match             62.0%;  Score 12.4;  DB 6;  Length 18;
  Best Local Similarity   92.9%;  Pred. No. 6e+05;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 CTTGCAGGAAGCGG 18
              || ||||||||||||
Db          3 CTGGCAGGAAGCGG 16


RESULT 13
AR098941/c
LOCUS       AR098941                  20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 77 from patent US 6077685.
ACCESSION   AR098941
VERSION     AR098941.1  GI:12808707
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Trofatter,J.A., MacCollin,M.M. and Gusella,J.F.
  TITLE     Tumor suppressor merlin and antibodies thereof
  JOURNAL   Patent: US 6077685-A 77 20-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             62.0%;  Score 12.4;  DB 6;  Length 20;
  Best Local Similarity   92.9%;  Pred. No. 5.9e+05;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CTCTTGCAGGAAGC 16
              |||||||||| |||
Db         15 CTCTTGCAGGTAGC 2


RESULT 14
AR164768/c
LOCUS       AR164768                  20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 79 from patent US 6274332.
ACCESSION   AR164768
VERSION     AR164768.1  GI:16237937
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Keating,M.T., Sanguinetti,M.C. and Splawski,I.
  TITLE     Mutations in the KCNE1 gene encoding human minK which cause
            arrhythmia susceptibility thereby establishing KCNE1 as an LQT gene
  JOURNAL   Patent: US 6274332-A 79 14-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             62.0%;  Score 12.4;  DB 6;  Length 20;
  Best Local Similarity   92.9%;  Pred. No. 5.9e+05;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 TGCAGGAAGCGGCT 20
              ||||||||||||| |
Db         18 TGCAGGAAGCGGAT 5


RESULT 15
BD222879/c
LOCUS       BD222879                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  KVLQT1-QT extension syndrome.
ACCESSION   BD222879
VERSION     BD222879.1  GI:33032649
KEYWORDS    JP 2002521045-A/77.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Keating,M.T., Sanguinetti,M.C., Karan,M.E., Landes,G.M.,
            Connors,T.D., Burn,T.C. and Splawski,I.
  TITLE     KVLQT1-QT extension syndrome
  JOURNAL   Patent: JP 2002521045-A 77 16-JUL-2002;
            UNIVERSITY OF UTAH RESEARCH FOUNDATION,GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002521045-A/77
            PD   16-JUL-2002
            PF   12-MAY-1999 JP 2000562052
            PR   29-JUL-1998 US    60/094477,17-AUG-1998 US    09/135010 PI
            MARK T KEATING,MICHAEL C SANGUINETTI,MARK E KARAN,GREGORY M  PI
            LANDES,
            PI   TIMOTHY D CONNORS,TIMOTHY C BURN,IGOR SPLAWSKI PC
            C12N15/09,A01K67/027,C07K14/46,C07K14/47,C07K16/18,C12N1/15, PC
            C12N1/19,
            PC
            C12N1/21,C12N5/10,C12P21/08,C12Q1/02,C12Q1/68,G01N33/15,G01N33/ PC
             50,
            PC   G01N33/53,G01N33/53,G01N33/566,G01N33/577,G01N33/58,G01N33/68,
            PC   C12N15/00,
            PC   C12N5/00
            CC   KVLQT1-QT extension syndrome
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             62.0%;  Score 12.4;  DB 6;  Length 20;
  Best Local Similarity   92.9%;  Pred. No. 5.9e+05;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 TGCAGGAAGCGGCT 20
              ||||||||||||| |
Db         18 TGCAGGAAGCGGAT 5


RESULT 16
I79781/c
LOCUS       I79781                    20 bp    DNA     linear   PAT 10-JUN-1998
DEFINITION  Sequence 77 from patent US 5707863.
ACCESSION   I79781
VERSION     I79781.1  GI:3208071
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Trofatter,J.A., MacCollin,M.M. and Gusella,J.F.
  TITLE     Tumor suppressor gene merlin
  JOURNAL   Patent: US 5707863-A 77 13-JAN-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
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ORIGIN

  Query Match             62.0%;  Score 12.4;  DB 6;  Length 20;
  Best Local Similarity   92.9%;  Pred. No. 5.9e+05;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CTCTTGCAGGAAGC 16
              |||||||||| |||
Db         15 CTCTTGCAGGTAGC 2


RESULT 17
AR218732/c
LOCUS       AR218732                 20 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 79 from patent US 6420124.
ACCESSION   AR218732
VERSION     AR218732.1  GI:23319627
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Keating,M.T., Sanguinetti,M.C., Curran,M.E., Landes,G.M.,
            Connors,T.D., Burn,T.C. and Splawski,I.
  TITLE     KVLQT1--a long qt syndrome gene
  JOURNAL   Patent: US 6420124-A 79 16-JUL-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             62.0%;  Score 12.4;  DB 6;  Length 20;
  Best Local Similarity   92.9%;  Pred. No. 5.9e+05;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 TGCAGGAAGCGGCT 20
              |||||||||||| |
Db         18 TGCAGGAAGCGGAT 5


RESULT 18
AR223147/c
LOCUS       AR223147                 20 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 79 from patent US 6432644.
ACCESSION   AR223147
VERSION     AR223147.1  GI:23331000
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Keating,M.T., Sanguinetti,M.C. and Splawski,I.
  TITLE     Mutations in the KCNE1 gene encoding human mink which cause
            arrhythmia susceptibility thereby establishing KCNE1 as an LQT gene
  JOURNAL   Patent: US 6432644-A 79 13-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             62.0%;  Score 12.4;  DB 6;  Length 20;
  Best Local Similarity   92.9%;  Pred. No. 5.9e+05;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 TGCAGGAAGCGGCT 20
              |||||||||||| |
Db         18 TGCAGGAAGCGGAT 5


RESULT 19
AR229909/c
LOCUS       AR229909                 20 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 79 from patent US 6451534.
ACCESSION   AR229909
VERSION     AR229909.1  GI:27269787
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Keating,M.T., Sanguinetti,M.C., Curran,M.E., Landes,G.M.,
            Connors,T.D., Burn,T.C. and Splawski,I.
  TITLE     KVLQT1--a long QT syndrome gene
  JOURNAL   Patent: US 6451534-A 79 17-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             62.0%;  Score 12.4;  DB 6;  Length 20;
  Best Local Similarity   92.9%;  Pred. No. 5.9e+05;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 TGCAGGAAGCGGCT 20
              |||||||||||| |
Db         18 TGCAGGAAGCGGAT 5


RESULT 20
AR262165/c
LOCUS       AR262165                 20 bp    DNA     linear   PAT 29-JAN-2003
DEFINITION  Sequence 79 from patent US 6323026.
ACCESSION   AR262165
VERSION     AR262165.1  GI:28073526
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Keating,M.T., Sanguinetti,M.C. and Splawski,I.
  TITLE     Mutations in the KCNE1 gene encoding human mink which cause
            arrhythmia susceptibility thereby establishing KCNE1 as an LQT gene
  JOURNAL   Patent: US 6323026-A 79 27-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             62.0%;  Score 12.4;  DB 6;  Length 20;
  Best Local Similarity   92.9%;  Pred. No. 5.9e+05;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 TGCAGGAAGCGGCT 20
              |||||||||||| |
Db         18 TGCAGGAAGCGGAT 5


RESULT 21
AR344603/c
LOCUS       AR344603                 20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 79 from patent US 6582913.
ACCESSION   AR344603
VERSION     AR344603.1  GI:33740672
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Keating,M.T., Sanguinetti,M.C., Curran,M.E., Landes,G.M.,
            Connors,T.D., Burn,T.C. and Splawski,I.
  TITLE     Diagnostic method for KVLQT1--a long QT syndrome gene
  JOURNAL   Patent: US 6582913-A 79 24-JUN-2003;
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FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             62.0%;  Score 12.4;  DB 6;  Length 20;
  Best Local Similarity   92.9%;  Pred. No. 5.9e+05;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 TGCAGGAAGCGGCT 20
              ||||||||||||| |
Db         18 TGCAGGAAGCGGAT 5


RESULT 22
CQ623374
LOCUS       CQ623374                  17 bp    DNA     linear   PAT 02-FEB-2004
DEFINITION  Sequence 8114 from Patent WO0192524.
ACCESSION   CQ623374
VERSION     CQ623374.1  GI:41673592
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
  TITLE     Myosin-like gene expressed in human heart and muscle
  JOURNAL   Patent: WO 0192524-A 8114 06-DEC-2001;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             61.0%;  Score 12.2;  DB 6;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 7.5e+05;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 TCTTGCAGGAAGCGGCT 20
              || |||  |||||||||
Db          1 TCCTGCCAGAAGCGGCT 17


RESULT 23
AR464437
LOCUS       AR464437                  17 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 8114 from patent US 6686188.
ACCESSION   AR464437
VERSION     AR464437.1  GI:42699494
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
  TITLE     Polynucleotide encoding a human myosin-like polypeptide expressed
            predominantly in heart and muscle
  JOURNAL   Patent: US 6686188-A 8114 03-FEB-2004;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             61.0%;  Score 12.2;  DB 6;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 7.5e+05;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 TCTTGCAGGAAGCGGCT 20
              || |||  |||||||||
Db          1 TCCTGCCAGAAGCGGCT 17


RESULT 24
AX039777/c
LOCUS       AX039777                  18 bp    DNA     linear   PAT 18-NOV-2000
DEFINITION  Sequence 166 from Patent WO0063441.
ACCESSION   AX039777
VERSION     AX039777.1  GI:11229806
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Herrnstadt,C. and Davis,R.E.
  TITLE     Single nucleotide polymorphisms in mitochondrial genes that segreg
            ate with alzheimer's disease
  JOURNAL   Patent: WO 0063441-A 166 26-OCT-2000;
            MITOKOR (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="PCR primer"
ORIGIN

  Query Match             61.0%;  Score 12.2;  DB 6;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 7.5e+05;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 ACTCTTGCAGGAAGCGG 18
              | |||||||| ||| |||
Db         17 ATTCTTGCACGAAACGG 1


RESULT 25
AX130162/c
LOCUS       AX130162                  19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 1380 from Patent WO0130362.
ACCESSION   AX130162
VERSION     AX130162.1  GI:14136467
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 1380 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Cdk-we-hu ribozyme binding site"
ORIGIN

  Query Match             61.0%;  Score 12.2;  DB 6;  Length 19;
  Best Local Similarity   82.4%;  Pred. No. 7.4e+05;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 ACTCTTGCAGGAAGCGG 18
              |||||| |  |||||||
Db         18 ACTCTTTCTAGAAGCGG 2
```

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RESULT 26
AX674695
LOCUS       AX674695                  17 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 3140 from Patent WO03004526.
ACCESSION   AX674695
VERSION     AX674695.1  GI:29333043
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
  JOURNAL   Patent: WO 03004526-A 3140 16-JAN-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             60.0%;  Score 12;  DB 6;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.4e+05;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 TCTTGCAGGAAG 15
              ||||||||||||
Db          3 TCTTGCAGGAAG 14


RESULT 27
AX728763/c
LOCUS       AX728763                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 397 from Patent WO03025175.
ACCESSION   AX728763
VERSION     AX728763.1  GI:30508106
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 397 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             60.0%;  Score 12;  DB 6;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.4e+05;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 ACTCTTGCAGGA 13
              ||||||||||||
Db         14 ACTCTTGCAGGA 3


RESULT 28
AR296765/c
LOCUS       AR296765                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 8500 from patent US 6537751.
ACCESSION   AR296765
VERSION     AR296765.1  GI:31684049
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 8500 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             60.0%;  Score 12;  DB 6;  Length 20;
  Best Local Similarity   75.0%;  Pred. No. 9.2e+05;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GACTCTTGCAGGAAGCGGCT 20
              |||| |||||  |||| | |
Db         20 GACTTTTGCACTAAGCAGAT 1


RESULT 29
BD259354
LOCUS       BD259354                  17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD259354
VERSION     BD259354.1  GI:33069124
KEYWORDS    JP 2002541795-A/7147.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 7147 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/7147
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Eukaryote'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             59.0%;  Score 11.8;  DB 6;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 1.2e+06;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GACTCTTGCAGGAAG 15
              |||| || |||||||
Db          3 GACTATTTCAGGAAG 17
```

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RESULT 30
BD259355
LOCUS       BD259355                 17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD259355
VERSION     BD259355.1  GI:33069125
KEYWORDS    JP 2002541795-A/7148.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 7148 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/7148
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
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            FT                   /organism='Eukaryote'.
FEATURES            Location/Qualifiers
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                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"
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Qy          1 GACTCTTGCAGGAAG 15
              |||| || |||||||
Db          2 GACTATTTCAGGAAG 16


RESULT 31
BD259356
LOCUS       BD259356                 17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD259356
VERSION     BD259356.1  GI:33069126
KEYWORDS    JP 2002541795-A/7149.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 7149 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/7149
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
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Qy          1 GACTCTTGCAGGAAG 15
              |||| || |||||||
Db          1 GACTATTTCAGGAAG 15


RESULT 32
AX214649/c
LOCUS       AX214649                 17 bp    RNA     linear   PAT 07-SEP-2001
DEFINITION  Sequence 91 from Patent WO0159103.
ACCESSION   AX214649
VERSION     AX214649.1  GI:15524692
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 91 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES            Location/Qualifiers
     source         1. .17
                    /organism="synthetic construct"
                    /mol_type="unassigned RNA"
                    /db_xref="taxon:32630"
                    /note="Nucleic Acid"
ORIGIN

  Query Match             59.0%;  Score 11.8;  DB 6;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 1.2e+06;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 TTGCAGGAAGCGGCT 20
              ||| | |||||||||
Db         16 TTGAAAGAAGCGGCT 2


RESULT 33
AX214650/c
LOCUS       AX214650                 17 bp    RNA     linear   PAT 07-SEP-2001
DEFINITION  Sequence 92 from Patent WO0159103.
ACCESSION   AX214650
VERSION     AX214650.1  GI:15524693
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
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            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 92 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"
ORIGIN

  Query Match            59.0%;  Score 11.8;  DB 6;  Length 17;
  Best Local Similarity  86.7%;  Pred. No. 1.2e+06;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 TTGCAGGAAGCGGCT 20
              ||| | |||||||||
Db         15 TTGAAAGAAGCGGCT 1


RESULT 34
AX215555/c
LOCUS       AX215555                  17 bp    RNA     linear   PAT 07-SEP-2001
DEFINITION  Sequence 997 from Patent WO0159103.
ACCESSION   AX215555
VERSION     AX215555.1  GI:15525598
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 997 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
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                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"
ORIGIN

  Query Match            59.0%;  Score 11.8;  DB 6;  Length 17;
  Best Local Similarity  86.7%;  Pred. No. 1.2e+06;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 TTGCAGGAAGCGGCT 20
              ||| | |||||||||
Db         17 TTGAAAGAAGCGGCT 3


RESULT 35
AX648385/c
LOCUS       AX648385                  17 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 225 from Patent EP1273660.
ACCESSION   AX648385
VERSION     AX648385.1  GI:29151203
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gu,Y.
  TITLE     Human sodium-hydrogen exchanger like protein 1
  JOURNAL   Patent: EP 1273660-A 225 08-JAN-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
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  Query Match            59.0%;  Score 11.8;  DB 6;  Length 17;
  Best Local Similarity  86.7%;  Pred. No. 1.2e+06;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 TCTTGCAGGAAGCGG 18
              || |||| |||||||
Db         17 TCATGCAAGAAGCGG 3


RESULT 36
AX648386/c
LOCUS       AX648386                  17 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 226 from Patent EP1273660.
ACCESSION   AX648386
VERSION     AX648386.1  GI:29151204
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gu,Y.
  TITLE     Human sodium-hydrogen exchanger like protein 1
  JOURNAL   Patent: EP 1273660-A 226 08-JAN-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
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  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 TCTTGCAGGAAGCGG 18
              || |||| |||||||
Db         16 TCATGCAAGAAGCGG 2


RESULT 37
AX648387/c
LOCUS       AX648387                  17 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 227 from Patent EP1273660.
ACCESSION   AX648387
VERSION     AX648387.1  GI:29151205
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gu,Y.
  TITLE     Human sodium-hydrogen exchanger like protein 1
  JOURNAL   Patent: EP 1273660-A 227 08-JAN-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
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ORIGIN

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Qy          4 TCTTGCAGGAAGCGG 18
              || |||| |||||||
Db         15 TCATGCAAGAAGCGG 1


RESULT 38
AR162450/c
LOCUS       AR162450                  20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 130 from patent US 6258600.
ACCESSION   AR162450
VERSION     AR162450.1  GI:16229633
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Zhang,H. and Cowsert,L.M.
  TITLE     Antisense modulation of caspase 8 expression
  JOURNAL   Patent: US 6258600-A 130 10-JUL-2001;
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             59.0%;  Score 11.8;  DB 6;  Length 20;
  Best Local Similarity   86.7%;  Pred. No. 1.2e+06;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GACTCTTGCAGGAAG 15
              || ||||| ||||||
Db         15 GAGTCTTGAAGGAAG 1


RESULT 39
AX116615/c
LOCUS       AX116615                  19 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 1738 from Patent WO0129262.
ACCESSION   AX116615
VERSION     AX116615.1  GI:14033557
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Picoult-Newburg,L. and Pohl,M.
  TITLE     Genotyping reagents, kits and methods of use thereof
  JOURNAL   Patent: WO 0129262-A 1738 26-APR-2001;
            Orchid BioSciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"
ORIGIN

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Qy          3 CTCTTGCAGGAAGCGGCT 20
              | | |||||| || ||||
Db         19 CCCATGCAGGTAGTGGCT 2


RESULT 40
AR067594/c
LOCUS       AR067594                  20 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1 from patent US 5851769.
ACCESSION   AR067594
VERSION     AR067594.1  GI:5998816
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Gray,J.W. and Weier,H.-U.G.
  TITLE     Quantitative DNA fiber mapping
  JOURNAL   Patent: US 5851769-A 1 22-DEC-1998;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
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ORIGIN

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Qy          1 GACTCTTGCAGGAAGCGG 18
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Db         20 GAGTACTGCAGGAAGAGG 3


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SUMMARIES

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	3	12.8	64.0	20	4	US-09-081-385-134	Sequence 134, App
c	4	12.4	62.0	20	1	US-08-171-718-77	Sequence 77, Appl
c	5	12.4	62.0	20	3	US-08-478-087-77	Sequence 77, Appl
c	6	12.4	62.0	20	3	US-09-135-020-79	Sequence 79, Appl
c	7	12.4	62.0	20	3	US-09-135-010A-79	Sequence 79, Appl
c	8	12.4	62.0	20	3	US-09-444-871-79	Sequence 79, Appl
c	9	12.4	62.0	20	3	US-09-597-735-79	Sequence 79, Appl
c	10	12.4	62.0	20	3	US-09-444-295-79	Sequence 79, Appl
c	11	12.4	62.0	20	3	US-09-597-732-79	Sequence 79, Appl
c	12	12.4	62.0	20	4	US-09-597-731-79	Sequence 79, Appl
	13	12.2	61.0	17	4	US-09-866-108A-8114	Sequence 8114, Ap
c	14	12.2	61.0	19	4	US-09-696-791-1380	Sequence 1380, Ap
c	15	12	60.0	20	4	US-09-422-978-8500	Sequence 8500, Ap
c	16	11.8	59.0	20	3	US-09-487-445-130	Sequence 130, App
c	17	11.6	58.0	20	2	US-08-534-479-1	Sequence 1, Appli
c	18	11.6	58.0	20	3	US-09-489-869-49	Sequence 49, Appl
c	19	11.6	58.0	20	4	US-09-596-248D-38	Sequence 38, Appl
	20	11.6	58.0	20	4	US-09-596-248D-39	Sequence 39, Appl
	21	11.6	58.0	20	4	US-09-972-115A-29	Sequence 29, Appl
	22	11.4	57.0	17	4	US-09-866-108A-115	Sequence 115, App
	23	11.4	57.0	17	4	US-09-866-108A-116	Sequence 116, App
	24	11.4	57.0	17	4	US-09-866-108A-117	Sequence 117, App
	25	11.4	57.0	17	4	US-09-866-108A-118	Sequence 118, App
	26	11.4	57.0	17	4	US-09-866-108A-119	Sequence 119, App
c	27	11.4	57.0	17	4	US-09-866-108A-6215	Sequence 6215, Ap
c	28	11.4	57.0	17	4	US-09-866-108A-6216	Sequence 6216, Ap
c	29	11.4	57.0	17	4	US-09-866-108A-6217	Sequence 6217, Ap
c	30	11.4	57.0	17	4	US-09-866-108A-6218	Sequence 6218, Ap
c	31	11.4	57.0	17	4	US-09-866-108A-6219	Sequence 6219, Ap
	32	11.4	57.0	18	2	US-09-256-496-10	Sequence 10, Appl
c	33	11.4	57.0	20	3	US-09-517-584A-11	Sequence 11, Appl
	34	11.4	57.0	20	3	US-09-467-082-27	Sequence 27, Appl
	35	11.4	57.0	20	3	US-09-658-687A-51	Sequence 51, Appl
	36	11.4	57.0	20	4	US-09-198-452A-6247	Sequence 6247, Ap
c	37	11.2	56.0	16	4	US-09-856-662-20	Sequence 20, Appl
	38	11.2	56.0	17	4	US-09-474-432B-429	Sequence 429, App
	39	11.2	56.0	17	4	US-09-476-387-428	Sequence 428, App
c	40	11.2	56.0	17	4	US-09-866-108A-7632	Sequence 7632, Ap
c	41	11.2	56.0	17	4	US-09-866-108A-7633	Sequence 7633, Ap
	42	11.2	56.0	17	4	US-09-866-108A-8113	Sequence 8113, Ap
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	45	11.2	56.0	20	3	US-09-428-583-39	Sequence 39, Appl
	46	11	55.0	20	1	US-07-977-284A-82	Sequence 82, Appl
	47	11	55.0	20	2	US-08-256-426B-82	Sequence 82, Appl
	48	11	55.0	20	4	US-09-954-560-16	Sequence 16, Appl
c	49	11	55.0	20	4	US-10-029-517-97	Sequence 97, Appl
	50	11	55.0	20	4	US-09-232-785-386	Sequence 386, App
	51	10.8	54.0	15	1	US-08-311-760A-57	Sequence 57, Appl
	52	10.8	54.0	15	1	US-08-311-760A-193	Sequence 193, App
	53	10.8	54.0	15	2	US-08-774-310-57	Sequence 57, Appl
	54	10.8	54.0	15	2	US-08-774-310-193	Sequence 193, App
	55	10.8	54.0	15	4	US-09-474-432B-142	Sequence 142, App
	56	10.8	54.0	15	4	US-09-476-387-142	Sequence 142, App
	57	10.8	54.0	17	3	US-08-985-162-216	Sequence 216, App
c	58	10.8	54.0	17	3	US-08-985-162-485	Sequence 485, App
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c	60	10.8	54.0	17	4	US-09-371-772B-4578	Sequence 4578, Ap
c	61	10.8	54.0	17	4	US-09-476-387-483	Sequence 483, App
	62	10.8	54.0	17	4	US-09-401-063-216	Sequence 216, App
c	63	10.8	54.0	17	4	US-09-401-063-485	Sequence 485, App
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	67	10.8	54.0	17	4	US-09-866-108A-8117	Sequence 8117, Ap
	68	10.8	54.0	18	4	US-09-877-177A-1	Sequence 1, Appli
	69	10.8	54.0	18	4	US-09-663-834A-47	Sequence 47, Appl
	70	10.8	54.0	19	3	US-09-676-610B-18	Sequence 18, Appl
	71	10.8	54.0	19	4	US-09-696-791-3517	Sequence 3517, Ap
	72	10.8	54.0	19	4	US-09-696-791-3518	Sequence 3518, Ap
c	73	10.8	54.0	20	2	US-08-809-297-39	Sequence 39, Appl
	74	10.8	54.0	20	3	US-09-226-012-30	Sequence 30, Appl
	75	10.8	54.0	20	3	US-09-487-368A-93	Sequence 93, Appl
	76	10.8	54.0	20	3	US-09-489-868A-35	Sequence 35, Appl
c	77	10.8	54.0	20	3	US-09-702-251-44	Sequence 44, Appl
c	78	10.8	54.0	20	3	US-09-844-634-173	Sequence 173, App
	79	10.8	54.0	20	4	US-09-629-644A-93	Sequence 93, Appl
c	80	10.8	54.0	20	4	US-09-595-684B-18	Sequence 18, Appl
c	81	10.8	54.0	20	4	US-09-198-452A-1521	Sequence 1521, Ap
	82	10.8	54.0	20	4	US-09-629-644A-93	Sequence 93, Appl
c	83	10.8	54.0	20	4	US-10-177-573-25	Sequence 25, Appl
c	84	10.6	53.0	17	3	US-08-679-645-821	Sequence 821, App
c	85	10.6	53.0	17	4	US-09-866-108A-6214	Sequence 6214, Ap
c	86	10.6	53.0	17	4	US-09-866-108A-7631	Sequence 7631, Ap
	87	10.6	53.0	17	4	US-09-866-108A-8112	Sequence 8112, Ap
c	88	10.6	53.0	18	3	US-09-161-244-25	Sequence 25, Appl
	89	10.6	53.0	19	4	US-09-747-391-210	Sequence 210, App
	90	10.6	53.0	20	1	US-07-940-242A-12	Sequence 12, Appl
	91	10.6	53.0	20	1	US-08-157-235-9	Sequence 9, Appli
	92	10.6	53.0	20	1	US-08-244-116B-25	Sequence 25, Appl
	93	10.6	53.0	20	1	US-08-832-172-3	Sequence 3, Appli
	94	10.6	53.0	20	2	US-08-242-580-3	Sequence 3, Appli
	95	10.6	53.0	20	2	US-08-470-426B-6	Sequence 6, Appli
	96	10.6	53.0	20	2	US-08-337-925-3	Sequence 3, Appli
c	97	10.6	53.0	20	3	US-09-167-921-29	Sequence 29, Appl
	98	10.6	53.0	20	3	US-08-647-924-44	Sequence 44, Appl
c	99	10.6	53.0	20	3	US-09-323-743-29	Sequence 29, Appl
c	100	10.6	53.0	20	4	US-09-216-393B-161	Sequence 161, App

ALIGNMENTS

RESULT 1
US-09-288-461-19
; Sequence 19, Application US/09288461
; Patent No. 6159694
; GENERAL INFORMATION:
; APPLICANT: Karras, James G.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
; TITLE OF INVENTION: Expression
; FILE REFERENCE: ISPH-0338
; CURRENT APPLICATION NUMBER: US/09/288,461
; CURRENT FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-288-461-19

Query Match 70.0%; Score 14; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAA 14
||||||||||||||
Db 7 GACTCTTGCAGGAA 20

RESULT 2
US-09-758-881-19
; Sequence 19, Application US/09758881
; Patent No. 6727064
; GENERAL INFORMATION:
; APPLICANT: Karras, James G
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
; TITLE OF INVENTION: Expression
; FILE REFERENCE: ISPH-0532
; CURRENT APPLICATION NUMBER: US/09/758,881
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/09054
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/288,461
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-758-881-19

Query Match 70.0%; Score 14; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAA 14
||||||||||||||
Db 7 GACTCTTGCAGGAA 20

RESULT 3
US-09-081-385-134
; Sequence 134, Application US/09081385
; Patent No. 6593456
; GENERAL INFORMATION:
; APPLICANT: Gatanaga, T.
; APPLICANT: Granger, G.A.
; TITLE OF INVENTION: Factors Altering Tumor Necrosis
; TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
; TITLE OF INVENTION: of Use Thereof
; NUMBER OF SEQUENCES: 154
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,385
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/964,747
; FILING DATE: 05-NOV-1997
; APPLICATION NUMBER: 60/030,761
; FILING DATE: 06-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Wu, Frank
; REGISTRATION NUMBER: 41,386
; REFERENCE/DOCKET NUMBER: 22000-20577.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 134:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-081-385-134

Query Match 64.0%; Score 12.8; DB 4; Length 20;
Best Local Similarity 87.5%; Pred. No. 3.8e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TCTTGCAGGAAGCGGC 19
|||| |||||||| ||
Db 1 TCTTCCAGGAAGCTGC 16

RESULT 4
US-08-171-718-77/c
; Sequence 77, Application US/08171718
; Patent No. 5707863
; GENERAL INFORMATION:
; APPLICANT: Trofatter, James A.
; APPLICANT: MacCollin, Mia M.
; APPLICANT: Gusella, James F.
; TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/171,718
;       FILING DATE:  22-DEC-1993
;       CLASSIFICATION:  436
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/108,808
;       FILING DATE:  19-AUG-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/022,034
;       FILING DATE:  25-FEB-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/026,063
;       FILING DATE:  04-MAR-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Brown, Anne
;       REGISTRATION NUMBER:  36,463
;       REFERENCE/DOCKET NUMBER:  0609.3850003
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202) 371-2600
;       TELEFAX:  (202) 371-2540
;   INFORMATION FOR SEQ ID NO:  77:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  20 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-171-718-77

  Query Match             62.0%;  Score 12.4;  DB 1;  Length 20;
  Best Local Similarity   92.9%;  Pred. No. 6e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CTCTTGCAGGAAGC 16
              |||||||||| |||
Db         15 CTCTTGCAGGTAGC 2


RESULT 5
US-08-478-087-77/c
; Sequence 77, Application US/08478087
; Patent No. 6077685
;  GENERAL INFORMATION:
;    APPLICANT:  Trofatter, James A.
;    APPLICANT:  MacCollin, Mia M.
;    APPLICANT:  Gusella, James F.
;    TITLE OF INVENTION:  Tumor Suppressor Gene Merlin and Uses
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  120
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1100 New York Avenue, N.W., Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/478,087
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/171,718
;      FILING DATE:  22-DEC-1993
;      APPLICATION NUMBER:  US 08/108,808
;      FILING DATE:  19-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/022,034
;      FILING DATE:  25-FEB-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/026,063
;      FILING DATE:  04-MAR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Anne
;      REGISTRATION NUMBER:  36,463
;      REFERENCE/DOCKET NUMBER:  0609.3850003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  77:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-478-087-77

  Query Match             62.0%;  Score 12.4;  DB 3;  Length 20;
  Best Local Similarity   92.9%;  Pred. No. 6e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CTCTTGCAGGAAGC 16
              |||||||||| |||
Db         15 CTCTTGCAGGTAGC 2


RESULT 6
US-09-135-020-79/c
; Sequence 79, Application US/09135020
; Patent No. 6274332
; GENERAL INFORMATION:
;  APPLICANT: Keating, Mark T.
;  APPLICANT: Sanguinetti, Michael C.
;  APPLICANT: Splawski, Igor
;  TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN minK WHICH
;  TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
;  TITLE OF INVENTION: KCNE1 AS AN LQT GENE
;  FILE REFERENCE: 2323-131
;  CURRENT APPLICATION NUMBER: US/09/135,020
;  CURRENT FILING DATE: 1998-08-17
;  EARLIER APPLICATION NUMBER: 08/921,068
;  EARLIER FILING DATE: 1997-08-29
;  EARLIER APPLICATION NUMBER: 08/739,383
;  EARLIER FILING DATE: 1996-10-29
;  EARLIER APPLICATION NUMBER: 60/019,014
;  EARLIER FILING DATE: 1995-12-22
;  EARLIER APPLICATION NUMBER: 60/094,477
;  EARLIER FILING DATE: 1998-07-29
;  NUMBER OF SEQ ID NOS: 114
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 79
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-135-020-79

  Query Match             62.0%;  Score 12.4;  DB 3;  Length 20;
  Best Local Similarity   92.9%;  Pred. No. 6e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 TGCAGGAAGCGGCT 20
              |||||||||||| |
Db         18 TGCAGGAAGCGGAT 5


RESULT 7
US-09-135-010A-79/c
; Sequence 79, Application US/09135010A
; Patent No. 6277978
; GENERAL INFORMATION:
```

```
;  APPLICANT:  Keating, Mark T.
;  APPLICANT:  Sanguinetti, Michael C.
;  APPLICANT:  Curran, Mark E.
;  APPLICANT:  Landes, Gregory M.
;  APPLICANT:  Connors, Timothy D.
;  APPLICANT:  Burn, Timothy C.
;  APPLICANT:  Splawski, Igor
;  TITLE OF INVENTION:  KVLQT1 - A LONG QT SYNDROME GENE
;  FILE REFERENCE:  2323-133
;  CURRENT APPLICATION NUMBER: US/09/135,010A
;  CURRENT FILING DATE:  1998-08-17
;  PRIOR APPLICATION NUMBER:  60/094,477
;  PRIOR FILING DATE:  1998-07-29
;  PRIOR APPLICATION NUMBER:  08/921,068
;  PRIOR FILING DATE:  1997-08-29
;  PRIOR APPLICATION NUMBER:  08/739,383
;  PRIOR FILING DATE:  1996-10-29
;  PRIOR APPLICATION NUMBER:  60/019,014
;  PRIOR FILING DATE:  1995-12-22
;  NUMBER OF SEQ ID NOS:  116
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 79
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-135-010A-79

  Query Match             62.0%;  Score 12.4;  DB 3;  Length 20;
  Best Local Similarity   92.9%;  Pred. No. 6e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 TGCAGGAAGCGGCT 20
              ||||||||||||| |
Db         18 TGCAGGAAGCGGAT 5


RESULT 8
US-09-444-871-79/c
; Sequence 79, Application US/09444871
; Patent No. 6323026
; GENERAL INFORMATION:
;  APPLICANT: Keating, Mark T.
;  APPLICANT: Sanguinetti, Michael C.
;  APPLICANT: Splawski, Igor
;  TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN minK WHICH
;  TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
;  TITLE OF INVENTION: KCNE1 AS AN LQT GENE
;  FILE REFERENCE: 2323-131
;  CURRENT APPLICATION NUMBER: US/09/444,871
;  CURRENT FILING DATE: 1999-11-22
;  EARLIER APPLICATION NUMBER: US 09/135,020
;  EARLIER FILING DATE: 1998-08-17
;  EARLIER APPLICATION NUMBER: 08/921,068
;  EARLIER FILING DATE: 1997-08-29
;  EARLIER APPLICATION NUMBER: 08/739,383
;  EARLIER FILING DATE: 1996-10-29
;  EARLIER APPLICATION NUMBER: 60/019,014
;  EARLIER FILING DATE: 1995-12-22
;  EARLIER APPLICATION NUMBER: 60/094,477
;  EARLIER FILING DATE: 1998-07-29
;  NUMBER OF SEQ ID NOS: 114
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 79
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-444-871-79

  Query Match             62.0%;  Score 12.4;  DB 3;  Length 20;
  Best Local Similarity   92.9%;  Pred. No. 6e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 TGCAGGAAGCGGCT 20
              ||||||||||||| |
Db         18 TGCAGGAAGCGGAT 5


RESULT 9
US-09-597-735-79/c
; Sequence 79, Application US/09597735
; Patent No. 6420124
; GENERAL INFORMATION:
;  APPLICANT: Keating, Mark T.
;  APPLICANT: Sanguinetti, Michael C.
;  APPLICANT: Curran, Mark E.
;  APPLICANT: Landes, Gregory M.
;  APPLICANT: Connors, Timothy D.
;  APPLICANT: Burn, Timothy C.
;  APPLICANT: Splawski, Igor
;  TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE
;  FILE REFERENCE: 2323-133
;  CURRENT APPLICATION NUMBER: US/09/597,735
;  CURRENT FILING DATE: 2000-06-19
;  EARLIER APPLICATION NUMBER: 09/135,010
;  EARLIER FILING DATE: 1998-08-17
;  EARLIER APPLICATION NUMBER: 60/094,477
;  EARLIER FILING DATE: 1998-07-29
;  EARLIER APPLICATION NUMBER: 08/921,068
;  EARLIER FILING DATE: 1997-08-29
;  EARLIER APPLICATION NUMBER: 08/739,383
;  EARLIER FILING DATE: 1996-10-29
;  EARLIER APPLICATION NUMBER: 60/019,014
;  EARLIER FILING DATE: 1995-12-22
;  NUMBER OF SEQ ID NOS: 116
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 79
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-597-735-79

  Query Match             62.0%;  Score 12.4;  DB 3;  Length 20;
  Best Local Similarity   92.9%;  Pred. No. 6e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 TGCAGGAAGCGGCT 20
              ||||||||||||| |
Db         18 TGCAGGAAGCGGAT 5


RESULT 10
US-09-444-295-79/c
; Sequence 79, Application US/09444295
; Patent No. 6432644
; GENERAL INFORMATION:
;  APPLICANT: Keating, Mark T.
;  APPLICANT:  Sanguinetti, Michael C.
;  APPLICANT:  Splawski, Igor
;  TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN minK WHICH
;  TITLE OF INVENTION:  CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
;  TITLE OF INVENTION:  KCNE1 AS AN LQT GENE
;  FILE REFERENCE: 2323-131
;  CURRENT APPLICATION NUMBER: US/09/444,295
;  CURRENT FILING DATE:  1999-11-22
;  PRIOR APPLICATION NUMBER: 09/135,020
;  PRIOR FILING DATE: 1998-08-17
;  PRIOR APPLICATION NUMBER: 08/921,068
;  PRIOR FILING DATE: 1997-08-29
;  PRIOR APPLICATION NUMBER: 08/739,383
;  PRIOR FILING DATE: 1996-10-29
;  PRIOR APPLICATION NUMBER: 60/019,014
;  PRIOR FILING DATE: 1995-12-22
;  PRIOR APPLICATION NUMBER: 60/094,477
;  PRIOR FILING DATE: 1998-07-29
;  NUMBER OF SEQ ID NOS: 114
;  SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 79
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-444-295-79

Query Match 62.0%; Score 12.4; DB 3; Length 20;
Best Local Similarity 92.9%; Pred. No. 6e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 TGCAGGAAGCGGCT 20
||||||||||||| |
Db 18 TGCAGGAAGCGGAT 5

RESULT 11
US-09-597-732-79/c
; Sequence 79, Application US/09597732
; Patent No. 6451534
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Curran, Mark E.
; APPLICANT: Landes, Gregory M.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE
; FILE REFERENCE: 2323-133
; CURRENT APPLICATION NUMBER: US/09/597,732
; CURRENT FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/135,010
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/094,477
; PRIOR FILING DATE: 1998-07-29
; PRIOR APPLICATION NUMBER: 08/921,068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/739,383
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/019,014
; PRIOR FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 79
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-597-732-79

Query Match 62.0%; Score 12.4; DB 3; Length 20;
Best Local Similarity 92.9%; Pred. No. 6e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 TGCAGGAAGCGGCT 20
||||||||||||| |
Db 18 TGCAGGAAGCGGAT 5

RESULT 12
US-09-597-731-79/c
; Sequence 79, Application US/09597731
; Patent No. 6582913
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Curran, Mark E.
; APPLICANT: Landes, Gregory M.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE
; FILE REFERENCE: 2323-133
; CURRENT APPLICATION NUMBER: US/09/597,731
; CURRENT FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/135,010
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 08/921,068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/739,383
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/019,014
; PRIOR FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 79
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-597-731-79

Query Match 62.0%; Score 12.4; DB 4; Length 20;
Best Local Similarity 92.9%; Pred. No. 6e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 TGCAGGAAGCGGCT 20
||||||||||||| |
Db 18 TGCAGGAAGCGGAT 5

RESULT 13
US-09-866-108A-8114
; Sequence 8114, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 8114
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-8114

Query Match 61.0%; Score 12.2; DB 4; Length 17;

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  Best Local Similarity   82.4%;  Pred. No. 7.4e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 TCTTGCAGGAAGCGGCT 20
              || |||  |||||||||
Db          1 TCCTGCCAGAAGCGGCT 17


RESULT 14
US-09-696-791-1380/c
; Sequence 1380, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
;  APPLICANT:  Robbins, Joan M.
;  APPLICANT:  Tritz, Richard
;  TITLE OF INVENTION:  RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
;  TITLE OF INVENTION:  SKIN AND EYE DISEASES
;  FILE REFERENCE:  480124.407
;  CURRENT APPLICATION NUMBER: US/09/696,791
;  CURRENT FILING DATE:  2000-10-25
;  NUMBER OF SEQ ID NOS:  4523
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 1380
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Cdk-we-hu ribozyme binding site
US-09-696-791-1380

  Query Match             61.0%;  Score 12.2;  DB 4;  Length 19;
  Best Local Similarity   82.4%;  Pred. No. 7.5e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 ACTCTTGCAGGAAGCGG 18
              |||||| |  |||||||
Db         18 ACTCTTTCTAGAAGCGG 2


RESULT 15
US-09-422-978-8500/c
; Sequence 8500, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT: Blumenfeld, Marta
;  APPLICANT: Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/09/422,978
;  CURRENT FILING DATE: 1999-10-20
;  EARLIER APPLICATION NUMBER: US 09/298,850
;  EARLIER FILING DATE: 1999-04-21
;  EARLIER APPLICATION NUMBER: US 60/109,732
;  EARLIER FILING DATE: 1998-11-23
;  EARLIER APPLICATION NUMBER: US 60/082,614
;  EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 8500
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..20
;   OTHER INFORMATION: downstream amplification primer 99-15968 for SEQ 635, in compleme
US-09-422-978-8500

  Query Match             60.0%;  Score 12;  DB 4;  Length 20;
  Best Local Similarity   75.0%;  Pred. No. 9.6e+03;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GACTCTTGCAGGAAGCGGCT 20
                |||| |||||  |||| | |
Db         20 GACTTTTGCACTAAGCAGAT 1


RESULT 16
US-09-487-445-130/c
; Sequence 130, Application US/09487445
; Patent No. 6258600
; GENERAL INFORMATION:
;  APPLICANT: Hong Zhang
;  APPLICANT: Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 8 EXPRESSION
;  FILE REFERENCE: RTS-0107
;  CURRENT APPLICATION NUMBER: US/09/487,445
;  CURRENT FILING DATE: 2000-01-19
;  NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 130
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-487-445-130

  Query Match             59.0%;  Score 11.8;  DB 3;  Length 20;
  Best Local Similarity   86.7%;  Pred. No. 1.2e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GACTCTTGCAGGAAG 15
              || ||||| ||||||
Db         15 GAGTCTTGAAGGAAG 1


RESULT 17
US-08-534-479-1/c
; Sequence 1, Application US/08534479
; Patent No. 5851769
;  GENERAL INFORMATION:
;    APPLICANT:  GRAY, JOE W.
;    APPLICANT:  WEIER, HEINZ-ULRICH G.
;    TITLE OF INVENTION:  QUANTITATIVE FIBER MAPPING
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MEDLEN & CARROLL
;      STREET:  220 MONTGOMERY STREET, SUITE 2200
;      CITY:  SAN FRANCISCO
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/534,479
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MACKNIGHT, KAMRIN T.
;      REGISTRATION NUMBER:  38,230
;      REFERENCE/DOCKET NUMBER:  LBL-01754
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-534-479-1
```

```
  Query Match             58.0%;  Score 11.6;  DB 2;  Length 20;
  Best Local Similarity   77.8%;  Pred. No. 1.5e+04;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GACTCTTGCAGGAAGCGG 18
              || |  ||||||||| ||
Db         20 GAGTACTGCAGGAAGAGG 3


RESULT 18
US-09-489-869-49/c
; Sequence 49, Application US/09489869A
; Patent No. 6268151
; GENERAL INFORMATION:
;  APPLICANT: Susan Murray
;  APPLICANT: Lex M. Cowsert
;  APPLICANT: Jacqueline Wyatt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF MACROPHAGE MIGRATION INHIBITORY FACTOR
;  FILE REFERENCE: RTS-0110
;  CURRENT APPLICATION NUMBER: US/09/489,869A
;  CURRENT FILING DATE: 2000-01-20
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 49
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-489-869-49

  Query Match             58.0%;  Score 11.6;  DB 3;  Length 20;
  Best Local Similarity   77.8%;  Pred. No. 1.5e+04;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 CTCTTGCAGGAAGCGGCT 20
              ||| | ||| |||| |||
Db         18 CTCCTACAGCAAGCTGCT 1


RESULT 19
US-09-596-248D-38/c
; Sequence 38, Application US/09596248D
; Patent No. 6599727
; GENERAL INFORMATION:
;  APPLICANT: Christenson, Erik
;  APPLICANT:  DeMaggio, Anthony J
;  APPLICANT:  Goldman, Phyllis S
;  APPLICANT:  McElligott, David L
;  TITLE OF INVENTION: Human Poly(ADP-Ribose) Polymerase 2 Materials and
;  TITLE OF INVENTION:  Methods
;  FILE REFERENCE: 27866/36544
;  CURRENT APPLICATION NUMBER: US/09/596,248D
;  CURRENT FILING DATE:  2000-06-16
;  PRIOR APPLICATION NUMBER: 60/139,543
;  PRIOR FILING DATE: 1999-06-16
;  NUMBER OF SEQ ID NOS: 68
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-596-248D-38

  Query Match             58.0%;  Score 11.6;  DB 4;  Length 20;
  Best Local Similarity   77.8%;  Pred. No. 1.5e+04;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GACTCTTGCAGGAAGCGG 18
              | ||||||  ||| ||||
Db         19 GGCTCTTGGTGGAGGCGG 2


RESULT 20
US-09-596-248D-39
; Sequence 39, Application US/09596248D
; Patent No. 6599727
; GENERAL INFORMATION:
;  APPLICANT: Christenson, Erik
;  APPLICANT:  DeMaggio, Anthony J
;  APPLICANT:  Goldman, Phyllis S
;  APPLICANT:  McElligott, David L
;  TITLE OF INVENTION: Human Poly(ADP-Ribose) Polymerase 2 Materials and
;  TITLE OF INVENTION:  Methods
;  FILE REFERENCE: 27866/36544
;  CURRENT APPLICATION NUMBER: US/09/596,248D
;  CURRENT FILING DATE:  2000-06-16
;  PRIOR APPLICATION NUMBER: 60/139,543
;  PRIOR FILING DATE: 1999-06-16
;  NUMBER OF SEQ ID NOS: 68
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-596-248D-39

  Query Match             58.0%;  Score 11.6;  DB 4;  Length 20;
  Best Local Similarity   77.8%;  Pred. No. 1.5e+04;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GACTCTTGCAGGAAGCGG 18
              | ||||||  ||| ||||
Db          2 GGCTCTTGGTGGAGGCGG 19


RESULT 21
US-09-972-115A-29
; Sequence 29, Application US/09972115A
; Patent No. 6599728
; GENERAL INFORMATION:
;  APPLICANT: Geron Corporation
;  APPLICANT:  Gregg, Morin B.
;  APPLICANT:  Walter, Funk D.
;  APPLICANT:  Mieczyslaw, Piatyszek A.
;  TITLE OF INVENTION: A Second Mammalian Telomerase
;  FILE REFERENCE: 080/003C
;  CURRENT APPLICATION NUMBER: US/09/972,115A
;  CURRENT FILING DATE:  2001-10-05
;  PRIOR APPLICATION NUMBER: US 60/128,577
;  PRIOR FILING DATE: 2000-04-10
;  PRIOR APPLICATION NUMBER: US 60/129,123
;  PRIOR FILING DATE: 1999-04-13
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Primer
US-09-972-115A-29

  Query Match             58.0%;  Score 11.6;  DB 4;  Length 20;
  Best Local Similarity   77.8%;  Pred. No. 1.5e+04;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GACTCTTGCAGGAAGCGG 18
              |||  |||| |||||| |
Db          3 GACAATTGCTGGAAGCTG 20
```

```
RESULT 22
US-09-866-108A-115
; Sequence 115, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108A
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 15755
;  SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 115
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108A-115

  Query Match             57.0%;  Score 11.4;  DB 4;  Length 17;
  Best Local Similarity   92.3%;  Pred. No. 1.9e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TCTTGCAGGAAGC 16
              ||| |||||||||
Db          5 TCTGGCAGGAAGC 17


RESULT 23
US-09-866-108A-116
; Sequence 116, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108A
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 15755
;  SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 116
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108A-116

  Query Match             57.0%;  Score 11.4;  DB 4;  Length 17;
  Best Local Similarity   92.3%;  Pred. No. 1.9e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TCTTGCAGGAAGC 16
              ||| |||||||||
Db          4 TCTGGCAGGAAGC 16


RESULT 24
US-09-866-108A-117
; Sequence 117, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108A
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
```

```
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 15755
;  SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 117
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108A-117

  Query Match             57.0%;  Score 11.4;  DB 4;  Length 17;
  Best Local Similarity   92.3%;  Pred. No. 1.9e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TCTTGCAGGAAGC 16
              ||| |||||||||
Db          3 TCTGGCAGGAAGC 15


RESULT 25
US-09-866-108A-118
; Sequence 118, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108A
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 15755
;  SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 118
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108A-118

  Query Match             57.0%;  Score 11.4;  DB 4;  Length 17;
  Best Local Similarity   92.3%;  Pred. No. 1.9e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TCTTGCAGGAAGC 16
              ||| |||||||||
Db          2 TCTGGCAGGAAGC 14


RESULT 26
US-09-866-108A-119
; Sequence 119, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108A
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 15755
;  SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 119
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108A-119

  Query Match             57.0%;  Score 11.4;  DB 4;  Length 17;
  Best Local Similarity   92.3%;  Pred. No. 1.9e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TCTTGCAGGAAGC 16
              ||| |||||||||
Db          1 TCTGGCAGGAAGC 13


RESULT 27
US-09-866-108A-6215/c
; Sequence 6215, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108A
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
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```
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 15755
;  SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6215
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108A-6215

  Query Match             57.0%;  Score 11.4;  DB 4;  Length 17;
  Best Local Similarity   92.3%;  Pred. No. 1.9e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GACTCTTGCAGGA 13
              |||| ||||||||
Db         17 GACTGTTGCAGGA 5


RESULT 28
US-09-866-108A-6216/c
; Sequence 6216, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108A
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 15755
;  SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6216
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108A-6216

  Query Match             57.0%;  Score 11.4;  DB 4;  Length 17;
  Best Local Similarity   92.3%;  Pred. No. 1.9e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GACTCTTGCAGGA 13
              |||| ||||||||
Db         16 GACTGTTGCAGGA 4


RESULT 29
US-09-866-108A-6217/c
; Sequence 6217, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108A
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 15755
;  SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6217
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108A-6217

  Query Match             57.0%;  Score 11.4;  DB 4;  Length 17;
  Best Local Similarity   92.3%;  Pred. No. 1.9e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GACTCTTGCAGGA 13
              |||| ||||||||
Db         15 GACTGTTGCAGGA 3
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RESULT 30
US-09-866-108A-6218/c
; Sequence 6218, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108A
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 15755
;  SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6218
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108A-6218

  Query Match             57.0%;  Score 11.4;  DB 4;  Length 17;
  Best Local Similarity   92.3%;  Pred. No. 1.9e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GACTCTTGCAGGA 13
              |||| ||||||||
Db         14 GACTGTTGCAGGA 2


RESULT 31
US-09-866-108A-6219/c
; Sequence 6219, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108A
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 15755
;  SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6219
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108A-6219

  Query Match             57.0%;  Score 11.4;  DB 4;  Length 17;
  Best Local Similarity   92.3%;  Pred. No. 1.9e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GACTCTTGCAGGA 13
              |||| ||||||||
Db         13 GACTGTTGCAGGA 1


RESULT 32
US-09-256-496-10
; Sequence 10, Application US/09256496
; Patent No. 5998206
; GENERAL INFORMATION:
;  APPLICANT: Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF G-APLHA-12 EXPRESSION
;  FILE REFERENCE: RTS-0056
;  CURRENT APPLICATION NUMBER: US/09/256,496
;  CURRENT FILING DATE: 1999-02-23
;  NUMBER OF SEQ ID NOS: 86
; SEQ ID NO 10
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-256-496-10

  Query Match             57.0%;  Score 11.4;  DB 2;  Length 18;
  Best Local Similarity   92.3%;  Pred. No. 1.9e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 GCAGGAAGCGGCT 20
              ||||| |||||||
Db          2 GCAGGCAGCGGCT 14


RESULT 33
US-09-517-584A-11/c
; Sequence 11, Application US/09517584A
; Patent No. 6187587
; GENERAL INFORMATION:
;  APPLICANT:      Ian Popoff
```

```
;  APPLICANT:  Vickie L. Brown-Driver
;  APPLICANT:  Lex M. Cowsert
;  TITLE OF INVENTION:      ANTISENSE MODULATION OF E2F TRANSCRIPTION FACTOR 1 EXPRESSIO
;  FILE REFERENCE:      RTS-0121
;  CURRENT APPLICATION NUMBER: US/09/517,584A
;  CURRENT FILING DATE:  2000-03-22
;  NUMBER OF SEQ ID NOS:      89
; SEQ ID NO 11
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Antisense Oligonucleotide
US-09-517-584A-11

  Query Match             57.0%;  Score 11.4;  DB 3;  Length 20;
  Best Local Similarity   92.3%;  Pred. No. 1.9e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 TTGCAGGAAGCGG 18
              ||||||| |||||
Db         13 TTGCAGGCAGCGG 1


RESULT 34
US-09-467-082-27
; Sequence 27, Application US/09467082
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PKA CATALYTIC SUBUNIT C-ALPHA EXPRESSION
;  FILE REFERENCE: RTS-0088
;  CURRENT APPLICATION NUMBER: US/09/467,082
;  CURRENT FILING DATE:  1999-12-17
;  NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 27
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Antisense Oligonucleotide
US-09-467-082-27

  Query Match             57.0%;  Score 11.4;  DB 3;  Length 20;
  Best Local Similarity   92.3%;  Pred. No. 1.9e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 CTTGCAGGAAGCG 17
              ||||||||| |||
Db          2 CTTGCAGGATGCG 14


RESULT 35
US-09-658-687A-51
; Sequence 51, Application US/09658687A
; Patent No. 6387699
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Jacqueline Wyatt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF A20 EXPRESSION
;  FILE REFERENCE: RTS-0141
;  CURRENT APPLICATION NUMBER: US/09/658,687A
;  CURRENT FILING DATE:  2000-09-08
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 51
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Antisense Oligonucleotide
US-09-658-687A-51

  Query Match             57.0%;  Score 11.4;  DB 3;  Length 20;
  Best Local Similarity   92.3%;  Pred. No. 1.9e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TCTTGCAGGAAGC 16
              |||||||||| ||
Db          2 TCTTGCAGGAGGC 14


RESULT 36
US-09-198-452A-6247
; Sequence 6247, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
;  APPLICANT: Griffais, R.
;  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
;  TITLE OF INVENTION:  thereof and uses thereof, in particular for the diagnosis, preve
;  TITLE OF INVENTION:  and treatment of infection
;  FILE REFERENCE: 9710-003-999
;  CURRENT APPLICATION NUMBER: US/09/198,452A
;  CURRENT FILING DATE:  1998-11-24
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 6247
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: Chlamydia pneumoniae
US-09-198-452A-6247

  Query Match             57.0%;  Score 11.4;  DB 4;  Length 20;
  Best Local Similarity   92.3%;  Pred. No. 1.9e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CTCTTGCAGGAAG 15
              || ||||||||||
Db          5 CTATTGCAGGAAG 17


RESULT 37
US-09-856-662-20/c
; Sequence 20, Application US/09856662
; Patent No. 6790616
; GENERAL INFORMATION:
;  APPLICANT: MORIBE, Toyoki et al.
;  TITLE OF INVENTION: Method for typing HLA class 1 genes
;  FILE REFERENCE: 0032-0261P
;  CURRENT APPLICATION NUMBER: US/09/856,662
;  CURRENT FILING DATE:  2001-05-24
;  PRIOR APPLICATION NUMBER: JP P1998-335151
;  PRIOR FILING DATE: 1998-11-26
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
;    LENGTH: 16
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence:DNA probe A402G
US-09-856-662-20

  Query Match             56.0%;  Score 11.2;  DB 4;  Length 16;
  Best Local Similarity   81.2%;  Pred. No. 2.4e+04;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 ACTCTTGCAGGAAGCG 17
              || |  ||||||||||
Db         16 ACCCGCGCAGGAAGCG 1


RESULT 38
US-09-474-432B-429
; Sequence 429, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
```

```
;  APPLICANT:  Beigelman, Leo
;  APPLICANT:  Burgin, Alex
;  APPLICANT:  Beaudry, Amber
;  APPLICANT:  Karpeisky, Alex
;  APPLICANT:  Adamic, Jasenka
;  APPLICANT:  Sweedler, David
;  APPLICANT:  Zinnen, Shawn
;  TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
;  FILE REFERENCE: MBHB00-831-B (247/276)
;  CURRENT APPLICATION NUMBER: US/09/474,432B
;  CURRENT FILING DATE:  1999-12-19
;  PRIOR APPLICATION NUMBER: US 60/064,866
;  PRIOR FILING DATE: 1997-11-05
;  PRIOR APPLICATION NUMBER: US 60/084,727
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: US 09/186,675
;  PRIOR FILING DATE: 1998-11-04
;  PRIOR APPLICATION NUMBER: US 09/301,511
;  PRIOR FILING DATE: 1999-04-28
;  NUMBER OF SEQ ID NOS: 1526
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 429
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-474-432B-429

  Query Match           56.0%;  Score 11.2;  DB 4;  Length 17;
  Best Local Similarity  68.8%;  Pred. No. 2.4e+04;
  Matches   11;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GACTCTTGCAGGAAGC 16
              |||:  :||||||| |
Db          2 GACUGCUGCAGGAAAC 17


RESULT 39
US-09-476-387-428
; Sequence 428, Application US/09476387
; Patent No. 6617438
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Beigelman, Leo
;  APPLICANT:  Beaudry, Amber
;  APPLICANT:  Karpeisky, Alex
;  APPLICANT:  Adamic, Jasenka Matulic
;  APPLICANT:  Sweedler, Dave
;  APPLICANT:  Zinnen, Shawn
;  TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleot
;  FILE REFERENCE: MBHB00-831-C (249/073)
;  CURRENT APPLICATION NUMBER: US/09/476,387
;  CURRENT FILING DATE:  2001-04-04
;  PRIOR APPLICATION NUMBER: 09/474,432
;  PRIOR FILING DATE: 1999-12-29
;  PRIOR APPLICATION NUMBER: 09/301,511
;  PRIOR FILING DATE: 1999-04-28
;  PRIOR APPLICATION NUMBER: 09/186,675
;  PRIOR FILING DATE: 1998-11-04
;  PRIOR APPLICATION NUMBER: 60/083,727
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/064,866
;  PRIOR FILING DATE: 1997-11-05
;  NUMBER OF SEQ ID NOS: 1524
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 428
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-476-387-428

  Query Match           56.0%;  Score 11.2;  DB 4;  Length 17;
  Best Local Similarity  68.8%;  Pred. No. 2.4e+04;
  Matches   11;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GACTCTTGCAGGAAGC 16
              |||:  :||||||| |
Db          2 GACUGCUGCAGGAAAC 17


RESULT 40
US-09-866-108A-7632/c
; Sequence 7632, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108A
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 15755
;  SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7632
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108A-7632

  Query Match           56.0%;  Score 11.2;  DB 4;  Length 17;
  Best Local Similarity  81.2%;  Pred. No. 2.4e+04;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 CTCTTGCAGGAAGCGG 18
              |||| |||||| || |
Db         17 CTCTAGCAGGACGCAG 2


Search completed: August  6, 2005, 16:30:01
Job time : 92 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 6, 2005, 09:48:11 ; Search time 231 Seconds
(without alignments)
512.532 Million cell updates/sec

Title: US-10-773-678-342
Perfect score: 20
Sequence: 1 gactcttgcaggaagcggct 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 2207178

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	2	14	70.0	20	6	AAS96785	Aas96785 Human STA
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c	4	13	65.0	15	4	AAF46591	Aaf46591 IGFBP3 ol
c	5	13	65.0	15	4	AAF46590	Aaf46590 IGFBP3 ol
c	6	13	65.0	15	4	AAF46589	Aaf46589 IGFBP3 ol
c	7	12.6	63.0	20	12	ADM92376	Adm92376 Pancreati
c	8	12.6	63.0	20	12	ADM14384	Adm14384 Human mPG
c	9	12.6	63.0	20	12	ADM14826	Adm14826 Human mPG
	10	12.4	62.0	17	10	ADB45311	Adb45311 Tumour su
	11	12.4	62.0	17	10	ACC52408	Acc52408 Human tum
	12	12.4	62.0	18	4	AAH39770	Aah39770 SNP speci
	13	12.4	62.0	18	12	ADE34379	Ade34379 Reverse p
c	14	12.4	62.0	20	2	AAQ71136	Aaq71136 Merlin ex
c	15	12.4	62.0	20	2	AAT90721	Aat90721 Human KVL
c	16	12.4	62.0	20	2	AAT91069	Aat91069 Human KVL
c	17	12.4	62.0	20	3	AAZ90745	Aaz90745 Human KVL
c	18	12.4	62.0	20	3	AAZ98975	Aaz98975 Mutant hu
c	19	12.4	62.0	20	13	ADR72365	Adr72365 Antisense
c	20	12.4	62.0	20	13	ADR72397	Adr72397 Antisense
	21	12.2	61.0	17	6	ABN08122	Abn08122 Human GDM
	22	12.2	61.0	17	13	ACN71212	Acn71212 Human GDM
c	23	12.2	61.0	18	3	AAC67455	Aac67455 Alzheimer
c	24	12.2	61.0	19	3	AAA83794	Aaa83794 cdk-we-hu
c	25	12.2	61.0	19	5	AAH58956	Aah58956 Cdk-we-hu
	26	12.2	61.0	19	13	ADT01798	Adt01798 Novel mut
c	27	12.2	61.0	20	2	AAT89003	Aat89003 Human mas
	28	12.2	61.0	20	2	AAZ02042	Aaz02042 PCR prime
c	29	12.2	61.0	20	2	AAX79782	Aax79782 PCR prime
c	30	12.2	61.0	20	8	ACC70917	Acc70917 Human cyt
c	31	12.2	61.0	20	12	ADM14320	Adm14320 Human mPG
c	32	12.2	61.0	20	12	ADM14505	Adm14505 Human mPG
c	33	12	60.0	15	4	AAF46592	Aaf46592 IGFBP3 ol
c	34	12	60.0	15	4	AAF46588	Aaf46588 IGFBP3 ol
c	35	12	60.0	17	8	ABT34760	Abt34760 Tumour su
	36	12	60.0	17	10	ACC54373	Acc54373 Human tum
c	37	12	60.0	19	10	ADF87984	Adf87984 Single nu
c	38	12	60.0	20	3	AAZ74144	Aaz74144 Human bia
	39	11.8	59.0	16	6	ABA02533	Aba02533 Lipoprote
	40	11.8	59.0	17	3	AAF07158	Aaf07158 Hammerhea
	41	11.8	59.0	17	3	AAF07156	Aaf07156 Hammerhea
	42	11.8	59.0	17	3	AAF07157	Aaf07157 Hammerhea
c	43	11.8	59.0	17	4	ABK00091	Abk00091 Human NOG
c	44	11.8	59.0	17	4	ABK00092	Abk00092 Human NOG
c	45	11.8	59.0	17	4	ABK00997	Abk00997 Human NOG
c	46	11.8	59.0	17	10	ADC03738	Adc03738 Human Na/
c	47	11.8	59.0	17	10	ADC03739	Adc03739 Human Na/
c	48	11.8	59.0	17	10	ADC03740	Adc03740 Human Na/
	49	11.8	59.0	19	10	ADF84039	Adf84039 Human bre
c	50	11.8	59.0	19	10	ADF83776	Adf83776 Human bre
c	51	11.8	59.0	20	5	AAD12444	Aad12444 Mouse cas
c	52	11.8	59.0	20	10	ADD25073	Add25073 Mouse cas
c	53	11.8	59.0	20	10	ABZ99166	Abz99166 Human PDE
c	54	11.8	59.0	20	11	ABD32197	Abd32197 Human PDE
c	55	11.8	59.0	20	12	ADK95604	Adk95604 Primer of
c	56	11.8	59.0	20	12	ADJ61051	Adj61051 Oligonucl
c	57	11.6	58.0	19	4	AAH38942	Aah38942 SNP speci
	58	11.6	58.0	19	12	ADK95770	Adk95770 Primer of
	59	11.6	58.0	20	3	AAC66842	Aac66842 Human tan
c	60	11.6	58.0	20	4	AAH42162	Aah42162 PCR prime
c	61	11.6	58.0	20	4	AAH23229	Aah23229 Human MMI
c	62	11.6	58.0	20	4	AAH20590	Aah20590 Human MTR
c	63	11.6	58.0	20	4	AAS07186	Aas07186 PCR prime
	64	11.6	58.0	20	5	AAC85334	Aac85334 cDNA prim
c	65	11.6	58.0	20	5	AAC85333	Aac85333 cDNA prim
c	66	11.6	58.0	20	5	AAF63986	Aaf63986 Human tan
	67	11.6	58.0	20	5	AAF63987	Aaf63987 Human tan
c	68	11.6	58.0	20	6	ABL51348	Abl51348 Human pho
c	69	11.6	58.0	20	8	ABZ25524	Abz25524 Human p53
c	70	11.6	58.0	20	10	ADG14241	Adg14241 Human PLA
c	71	11.6	58.0	20	10	ADH93238	Adh93238 Human gen
c	72	11.6	58.0	20	12	ADM14153	Adm14153 Human mPG
c	73	11.6	58.0	20	13	ADR46348	Adr46348 Mouse RS1
c	74	11.4	57.0	16	6	AAL47190	Aal47190 Human rhe
	75	11.4	57.0	17	4	AAF57367	Aaf57367 Murine Cd
	76	11.4	57.0	17	6	ABN00127	Abn00127 Human GDM
c	77	11.4	57.0	17	6	ABN06225	Abn06225 Human GDM
c	78	11.4	57.0	17	6	ABN06223	Abn06223 Human GDM
c	79	11.4	57.0	17	6	ABN06227	Abn06227 Human GDM
	80	11.4	57.0	17	6	ABN00123	Abn00123 Human GDM
c	81	11.4	57.0	17	6	ABN06224	Abn06224 Human GDM
	82	11.4	57.0	17	6	ABN00125	Abn00125 Human GDM
	83	11.4	57.0	17	6	ABN00124	Abn00124 Human GDM
	84	11.4	57.0	17	6	ABN00126	Abn00126 Human GDM
c	85	11.4	57.0	17	6	ABN06226	Abn06226 Human GDM
c	86	11.4	57.0	17	13	ACN69313	Acn69313 Human GDM
	87	11.4	57.0	17	13	ACN63215	Acn63215 Human GDM
c	88	11.4	57.0	17	13	ACN69315	Acn69315 Human GDM
c	89	11.4	57.0	17	13	ACN69316	Acn69316 Human GDM
c	90	11.4	57.0	17	13	ACN69317	Acn69317 Human GDM
	91	11.4	57.0	17	13	ACN63213	Acn63213 Human GDM
	92	11.4	57.0	17	13	ACN63217	Acn63217 Human GDM
	93	11.4	57.0	17	13	ACN63216	Acn63216 Human GDM

c	94	11.4	57.0	17	13	ACN69314	Acn69314 Human GDM
	95	11.4	57.0	17	13	ACN63214	Acn63214 Human GDM
	96	11.4	57.0	18	3	AAZ57670	Aaz57670 Human G-a
	97	11.4	57.0	20	2	AAX96921	Aax96921 PCR prime
c	98	11.4	57.0	20	3	AAC72420	Aac72420 Single nu
	99	11.4	57.0	20	4	AAA54448	Aaa54448 Primer fo
c	100	11.4	57.0	20	4	AAF91296	Aaf91296 Human E2F

ALIGNMENTS

RESULT 1
AAC93168
ID AAC93168 standard; DNA; 20 BP.
XX
AC AAC93168;
XX
DT 15-FEB-2001 (first entry)
XX
DE Human STAT3 phosphorothioate antisense oligonucleotide SEQ ID NO:19.
XX
KW Human; mouse; STAT3; phosphorothioate; antisense oligonucleotide;
KW modulation; signal transducer and activator of transcription;
KW DNA-binding protein; signal transduction; inhibition; apoptosis;
KW inflammatory disease; cancer; antiinflammatory; antirheumatic;
KW cytostatic; immunostimulatory; rheumatoid arthritis; leukaemia; myeloma;
KW melanoma; lymphoma; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO200061602-A1.
XX
PD 19-OCT-2000.
XX
PF 06-APR-2000; 2000WO-US009054.
XX
PR 08-APR-1999; 99US-00288461.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Karras JG;
XX
DR WPI; 2000-619223/59.
XX
PT New antisense compound for inhibiting the expression of signal transducer
PT and activator of transcription 3 (STAT3) in cells or tissues and treating
PT diseases or condition associated with STAT3, such as rheumatoid arthritis
PT and cancer.
XX
PS Example 2; Page 46; 104pp; English.
XX
CC The present invention describes an antisense compound (I), 8 to 30
CC nucleobases in length, that is targeted to a nucleic acid molecule
CC encoding STAT3 (Signal Transducer and Activator of Transcription) and
CC which inhibits the expression of it. (I) has antiinflammatory,
CC antirheumatic, cytostatic and immunostimulatory activities. (I) is used
CC for inhibiting the expression of STAT3 in cells or tissues, treating an
CC animal having a disease or condition associated with STAT3 or a human
CC having a disease or condition characterised by a reduction in apoptosis,
CC and inducing apoptosis in a cell. Diseases or conditions that are treated
CC are rheumatoid arthritis, cancer of the breast, prostate, brain, head
CC and/or neck, leukaemia, myeloma, melanoma or lymphoma. (I) can also be
CC used for diagnostic methods in detecting and determining the role of
CC STAT3 in various cell functions, physiological processes and conditions
CC and for diagnosing the conditions associated with expression of STAT3.
CC (I) can be used alone or with other drugs as an immunostimulator. (I) is
CC used in sandwich and colourimetric assays, involving enzyme conjugation
CC and radiolabeling and is used in diagnostic kits. AAC93150 encodes human
CC STAT3 and AAC93231 encodes mouse STAT3 as given in the exemplification of
CC the present invention. AAC93151 to AAC93230 and AAC93232 to AAC93299
CC represent STAT3 phosphorothioate antisense oligonucleotides, and AAC93300
CC represents a mismatch control oligonucleotide which are used in example
CC from the present invention
XX
SQ Sequence 20 BP; 6 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 70.0%; Score 14; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAA 14
||||||||||||||
Db 7 GACTCTTGCAGGAA 20

RESULT 2
AAS96785
ID AAS96785 standard; DNA; 20 BP.
XX
AC AAS96785;
XX
DT 26-FEB-2002 (first entry)
XX
DE Human STAT3 antisense phosphorothioate oligodeoxynucleotide #18.
XX
KW STAT3; human; signal transducer and activator of transcription; ss; STAT;
KW antisense gene therapy; Fas-mediated apoptosis; inflammatory disease;
KW autoimmune disease; rheumatoid arthritis; cancer; breast; prostate; head;
KW neck; brain; leukaemia; myeloma; melanoma; lymphoma; apoptosis;
KW antiinflammatory; immunosuppressive; antirheumatic; antiarthritic;
KW cytostatic.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US2001029250-A1.
XX
PD 11-OCT-2001.
XX
PF 11-JAN-2001; 2001US-00758881.
XX
PR 08-APR-1999; 99US-00288461.
PR 06-APR-2000; 2000WO-US009054.
XX
PA (KARR/) KARRAS J G.
XX
PI Karras JG;
XX
DR WPI; 2002-009991/01.
XX
PT Novel antisense compound useful for treating and diagnosing inflammatory
PT diseases and cancers, is targeted to a nucleic acid molecule encoding
PT signal transducer and activator of transcription proteins.
XX
PS Example 2; Page 13; 21pp; English.
XX
CC The invention relates to antisense compounds targeted to a nucleic acid
CC molecule encoding a signal transducer and activator of transcription
CC (STAT) protein, specifically STAT3, where the antisense compounds inhibit
CC the expression of STAT3. The antisense sequences are useful for
CC inhibiting the expression of STAT3 in cells or tissues, inducing Fas-
CC mediated apoptosis in cells, and sensitising cells to apoptosis. They are
CC also useful for treating an animal having a disease or condition
CC associated with STAT3. These disorders include inflammatory or autoimmune
CC disease, particularly rheumatoid arthritis, cancers, such as those of the
CC breast, prostate, brain and head and neck and leukaemias, myelomas,
CC melanomas and lymphomas. Also treatable are human diseases or conditions
CC characterised by a reduction in apoptosis or an insensitivity to
CC apoptotic signals. The sequences of the invention can be used in clinical
CC research, for detecting and determining the role of STAT3 in various cell
CC functions and physiological processes and for diagnosing conditions
CC associated with the expression of STAT3. The sequences represent cDNA
CC encoding human STAT3 and human STAT3 oligonucleotides
XX
SQ Sequence 20 BP; 6 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

```
  Query Match             70.0%;  Score 14;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GACTCTTGCAGGAA 14
              ||||||||||||||
Db          7 GACTCTTGCAGGAA 20
```

RESULT 3
ADM14825/c
ID ADM14825 standard; DNA; 20 BP.
XX
AC ADM14825;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:1012.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key   Location/Qualifiers
FT modified_base   1. .20
FT   /*tag= b
FT   /mod_base= OTHER
FT   /note= "phosphorothioate linkages and all cytidine
FT   residues are 5-methylcytidines"
FT modified_base   1. .5
FT   /*tag= a
FT   /mod_base= OTHER
FT   /note= "2'-O-methocyethyls"
FT modified_base   16. .20
FT   /*tag= c
FT   /mod_base= OTHER
FT   /note= "2'-O-methoxyethyls"
XX
PN WO2004028458-A2.
XX
PD 08-APR-2004.
XX
PF 25-SEP-2003; 2003WO-US030374.
XX
PR 25-SEP-2002; 2002US-0413549P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Gierse JK;
XX
DR WPI; 2004-305094/28.
XX
PT New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischemia.
XX
PS Claim 4; SEQ ID NO 1012; 132pp; English.
XX
CC The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC human mPGES-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGES-1. MPGES-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antidiabetic, immunomodulator, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

```
  Query Match             68.0%;  Score 13.6;  DB 12;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 8.6e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GACTCTTGCAGGAAGCGGCT 20
              || || |||| |||| ||||
Db         20 GATTCCTGCACGAAGTGGCT 1
```

RESULT 4
AAF46591/c
ID AAF46591 standard; DNA; 15 BP.
XX
AC AAF46591;
XX
DT 30-MAR-2001 (first entry)
XX
DE IGFBP3 oligonucleotide #11.
XX
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU000693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
PA (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI Wraight CJ, Werther GA, Edmondson SR;
XX
DR WPI; 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
PS Example 7; Page 44; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,

```
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 1 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             65.0%;  Score 13;  DB 4;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+04;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 GCAGGAAGCGGCT 20
              |||||||||||||
Db         13 GCAGGAAGCGGCT 1


RESULT 5
AAF46590/c
ID   AAF46590 standard; DNA; 15 BP.
XX
AC   AAF46590;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGFBP3 oligonucleotide #10.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 7; Page 44; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 1 A; 8 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             65.0%;  Score 13;  DB 4;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+04;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 GCAGGAAGCGGCT 20
              |||||||||||||
Db         14 GCAGGAAGCGGCT 2


RESULT 6
AAF46589/c
ID   AAF46589 standard; DNA; 15 BP.
XX
AC   AAF46589;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGFBP3 oligonucleotide #9.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 7; Page 44; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
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CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 1 A; 8 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             65.0%;  Score 13;  DB 4;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+04;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 GCAGGAAGCGGCT 20
              |||||||||||||
Db         15 GCAGGAAGCGGCT 3


RESULT 7
ADM92376/c
ID   ADM92376 standard; DNA; 20 BP.
XX
AC   ADM92376;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Pancreatic cancer related RT-PCR forward primer SEQ ID NO:13.
XX
KW   pancreatic cancer; diagnosis; pancreatic cancer-associated gene;
KW   cytostatic; vaccine; gene therapy; human; reverse transcription; PCR;
KW   primer; ss; semi-quantitative RT-PCR experiment.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2004031412-A2.
XX
PD   15-APR-2004.
XX
PF   17-SEP-2003; 2003WO-JP011817.
XX
PR   30-SEP-2002; 2002US-0414872P.
PR   28-FEB-2003; 2003US-0450889P.
XX
PA   (ONCO-) ONCOTHERAPY SCI INC.
PA   (UYTY ) UNIV TOKYO.
XX
PI   Nakamura Y,  Katagiri T;
XX
DR   WPI; 2004-330205/30.
XX
PT   Diagnosing pancreatic cancer (PNC) comprises determining a level of
PT   expression of a PNC-associated gene in a patient derived biological
PT   sample.
XX
PS   Example 1; SEQ ID NO 13; 152pp; English.
XX
CC   The present invention describes a method for diagnosing pancreatic cancer
CC   (PNC) or a predisposition to developing PNC in a subject. The method
CC   comprises determining a level of expression of a PNC-associated gene in a
CC   patient derived biological sample, where an increase or decrease of the
CC   level compared to a normal control level of the gene indicates that the
CC   subject suffers from or is at risk of developing PNC. Also described: (1)
CC   a PNC reference expression profile, comprising a pattern of gene
CC   expression of two or more genes, i.e. PNC 1-605 or PNC 850-866 and PNC
CC   894-906; (2) a method of screening for a compound for treating or
CC   preventing PNC or malignant PNC; (3) a kit comprising a detection reagent
CC   which binds to two or more nucleic acid sequences, i.e. PNC 1-605 or PNC
CC   850-866 and PNC 894-906 or the encoded polypeptides; (4) an array
CC   comprising two or more nucleic acids which bind to one or more nucleic
CC   acid sequences, i.e. PNC 1-605 or PNC 850-866 and PNC 894-906; (5) a
CC   method of treating or preventing PNC in a subject; (6) a composition, for
CC   treating or preventing PNC, comprising a pharmaceutical amount of: (a) an
CC   antisense polynucleotide or small interfering RNA against a
CC   polynucleotide, i.e. PNC 1-259, PNC 606-640 and PNC 682-741 or PNC 850-
CC   933; (b) an antibody or antibody fragment that binds to a protein encoded
CC   by any one gene, i.e. PNC 1-259, PNC 606-640 and PNC 682-741 or PNC 850-
CC   893; or (c) the compound obtained by the method of (2) as an active
CC   ingredient and a pharmaceutical carrier; and (7) a method of predicting
CC   recurrence of PNC. The compounds have cytostatic activity, and can be
CC   used in vaccines and in gene therapy. The method is useful in diagnosing
CC   PNC or a predisposition to developing PNC in a subject. The methods,
CC   compounds and compositions are useful in treating or preventing PNC. The
CC   polypeptides are useful as vaccines against PNC. The present sequence
CC   represents a reverse transcription (RT) PCR primer used in semi-
CC   quantitative RT-PCR experiments related to the diagnosis of PNC, which is
CC   used in an example from the present invention.
XX
SQ   Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

  Query Match             63.0%;  Score 12.6;  DB 12;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 2.6e+04;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 ACTCTTGCAGGAAGCGGCT 20
              | |||  |||||||| |||
Db         20 AATCTCCCAGGAAGCTGCT 2


RESULT 8
ADM14384/c
ID   ADM14384 standard; DNA; 20 BP.
XX
AC   ADM14384;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:571.
XX
KW   chimeric; antisense oligonucleotide; phosphorothioate; human;
KW   microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW   microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic;
KW   immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW   neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW   immunomodulatory; cardiovascular; gene therapy; inflammation;
KW   Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW   reperfusion injury; ophthalmic disorder; immunological disorder;
KW   cardiovascular disorder; neurological disorder; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages and all cytidine
FT                   residues are 5-methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methocyethyls"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyls"
XX
PN   WO2004028458-A2.
XX
PD   08-APR-2004.
XX
PF   25-SEP-2003; 2003WO-US030374.
XX
PR   25-SEP-2002; 2002US-0413549P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Gierse JK;
XX
DR   WPI; 2004-305094/28.
```

```
XX
PT   New antisense compound, having a sequence targeted to a nucleic acid
PT   encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT   inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT   ischemia.
XX
PS   Claim 4; SEQ ID NO 571; 132pp; English.
XX
CC   The present sequence represents a chimeric antisense oligonucleotide
CC   targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC   human mPGES-1 gene is located on chromosome 9, more specifically to
CC   9q34.3. The present invention also describes: (1) antisense compounds,
CC   having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC   mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC   inhibits its expression; (2) a method of inhibiting the expression of
CC   mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC   having a disease or condition associated with mPGES-1. MPGES-1 chimeric
CC   antisense oligonucleotides and antisense compounds have cytostatic,
CC   antidiabetic, immunomodulator, cardiant, neuroprotective,
CC   antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC   ophthalmological, immunomodulatory and cardiovascular activities, and can
CC   be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC   can be used for preparing a composition for treating a disease or
CC   condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC   disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC   ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ   Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             63.0%;  Score 12.6;  DB 12;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 2.6e+04;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GACTCTTGCAGGAAGCGGC 19
              || || |||| |||| |||
Db         19 GATTCCTGCACGAAGTGGC 1


RESULT 9
ADM14826/c
ID   ADM14826 standard; DNA; 20 BP.
XX
AC   ADM14826;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:1013.
XX
KW   chimeric; antisense oligonucleotide; phosphorothioate; human;
KW   microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW   microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic;
KW   immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW   neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW   immunomodulatory; cardiovascular; gene therapy; inflammation;
KW   Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW   reperfusion injury; ophthalmic disorder; immunological disorder;
KW   cardiovascular disorder; neurological disorder; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages and all cytidine
FT                   residues are 5-methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methocyethyls"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyls"
XX
PN   WO2004028458-A2.
XX
PD   08-APR-2004.
XX
PF   25-SEP-2003; 2003WO-US030374.
XX
PR   25-SEP-2002; 2002US-0413549P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Gierse JK;
XX
DR   WPI; 2004-305094/28.
XX
PT   New antisense compound, having a sequence targeted to a nucleic acid
PT   encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT   inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT   ischemia.
XX
PS   Claim 4; SEQ ID NO 1013; 132pp; English.
XX
CC   The present sequence represents a chimeric antisense oligonucleotide
CC   targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC   human mPGES-1 gene is located on chromosome 9, more specifically to
CC   9q34.3. The present invention also describes: (1) antisense compounds,
CC   having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC   mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC   inhibits its expression; (2) a method of inhibiting the expression of
CC   mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC   having a disease or condition associated with mPGES-1. MPGES-1 chimeric
CC   antisense oligonucleotides and antisense compounds have cytostatic,
CC   antidiabetic, immunomodulator, cardiant, neuroprotective,
CC   antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC   ophthalmological, immunomodulatory and cardiovascular activities, and can
CC   be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC   can be used for preparing a composition for treating a disease or
CC   condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC   disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC   ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ   Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             63.0%;  Score 12.6;  DB 12;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 2.6e+04;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 ACTCTTGCAGGAAGCGGCT 20
              | || |||| |||| ||||
Db         20 ATTCCTGCACGAAGTGGCT 2


RESULT 10
ADB45311
ID   ADB45311 standard; DNA; 17 BP.
XX
AC   ADB45311;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Tumour suppression/reversion associated nucleotide #5634.
XX
KW   cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW   primer; probe; tumour suppression; tumour reversion; apoptosis;
KW   virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW   diagnosis.
XX
OS   Homo sapiens.
XX
PN   WO2003040369-A2.
XX
```

PD 15-MAY-2003.
XX
PF 17-SEP-2002; 2002WO-IB004219.
XX
PR 17-SEP-2001; 2001FR-00011981.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-441574/41.
XX
PT New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
PS Disclosure; Page 690; 771pp; French.
XX
CC The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX
SQ Sequence 17 BP; 6 A; 2 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 62.0%; Score 12.4; DB 10; Length 17;
Best Local Similarity 92.9%; Pred. No. 3.3e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TCTTGCAGGAAGCG 17
||||||||||||| |
Db 3 TCTTGCAGGAAGAG 16

RESULT 11
ACC52408
ID ACC52408 standard; DNA; 17 BP.
XX
AC ACC52408;
XX
DT 27-JUN-2003 (first entry)
XX
DE Human tumour suppressor sequence #1175.
XX
KW ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
KW tumour regression; apoptosis; virus resistance; diagnosis;
KW cellular degeneration.
XX
OS Homo sapiens.
XX
PN FR2826373-A1.
XX
PD 27-DEC-2002.
XX
PF 20-JUN-2001; 2001FR-00008139.
XX
PR 20-JUN-2001; 2001FR-00008139.
XX
PA (MOLE-) MOLECULAR ENGINES LAB SA.
XX
PI Tuijnder M, Telerman A, Amson R;
XX
DR WPI; 2003-250498/25.
XX
PT New nucleic acid sequences associated with tumor suppression, regression,
PT apoptosis or virus resistance are useful to diagnose and treat viral
PT disease, development of tumor cells and cell degeneration.
XX
PS Claim 1; Page 311; 798pp; French.
XX
CC This sequence represents an isolated nucleic acid sequence associated
CC with tumour suppression or regression, apoptosis or virus resistance. The
CC invention relates to these sequences or sequences having at least 80%
CC identity to them, and polypeptides encoded by the sequences or
CC polypeptides having 80% identity to the polypeptide sequences. The
CC invention is used to diagnose or treat viral disease or disease
CC characterized by development of tumour cells or cellular degeneration
XX
SQ Sequence 17 BP; 4 A; 4 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 62.0%; Score 12.4; DB 10; Length 17;
Best Local Similarity 92.9%; Pred. No. 3.3e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 TGCAGGAAGCGGCT 20
| ||||||||||||
Db 3 TCCAGGAAGCGGCT 16

RESULT 12
AAH39770
ID AAH39770 standard; DNA; 18 BP.
XX
AC AAH39770;
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific lower PCR primer SEQ ID 2566.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200129262-A2.
XX
PD 26-APR-2001.
XX
PF 13-OCT-2000; 2000WO-US028436.
XX
PR 15-OCT-1999; 99US-0160096P.
XX
PA (ORCH-) ORCHID BIOSCIENCES INC.
XX
PI Picoult-Newburg L, Pohl M;
XX
DR WPI; 2001-290930/30.
XX
PT New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.
XX
PS Claim 1; Page 63; 83pp; English.
XX
CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking

```
CC   sites of single nucleotide polymorphisms SNPs. The present invention
CC   includes kits for determining the presence or absence of a SNP, using the
CC   oligonucleotides of the invention. The PCR primers are used to amplify a
CC   SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC   The oligonucleotides are useful for genotyping a nucleic acid sample by
CC   performing a single-nucleotide primer extension reaction. The
CC   oligonucleotides are useful for determining the presence, absence or
CC   identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC   assess by association analysis the genotype of an individual or group of
CC   individuals, having a pathological phenotypic trait suspected of being
CC   caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC   agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC   dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC   osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC   traits also include symptoms of or susceptibility to multifactorial
CC   disease of which a component is or may be genetic such as autoimmune
CC   diseases, including, rheumatoid arthritis, multiple sclerosis,
CC   inflammation, cancer, nervous system diseases and infection by pathogenic
CC   microorganism. The method is also useful in forensic investigations and
CC   paternity analysis. The present sequence represents a PCR primer specific
CC   for a human SNP containing DNA sequence
XX
SQ   Sequence 18 BP; 4 A; 4 C; 9 G; 1 T; 0 U; 0 Other;

  Query Match             62.0%;  Score 12.4;  DB 4;  Length 18;
  Best Local Similarity   92.9%;  Pred. No. 3.3e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 CTTGCAGGAAGCGG 18
              || ||||||||||||
Db          3 CTGGCAGGAAGCGG 16


RESULT 13
ADE34379
ID   ADE34379 standard; DNA; 18 BP.
XX
AC   ADE34379;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Reverse primer P4.
XX
KW   Helicobacter pylori; gastric carcinoma; Lewis antigen; polymorphism; PCR;
KW   primer; ss.
XX
OS   Unidentified.
XX
PN   WO2003080840-A1.
XX
PD   02-OCT-2003.
XX
PF   26-MAR-2002; 2002WO-CN000199.
XX
PR   26-MAR-2002; 2002WO-CN000199.
XX
PA   (UYPE-) UNIV PEKING SCHOOL ONCOLOGY.
XX
PI   Ke Y,  Jiang J,  Ning T,  Lu G,  You W,  Pan K;
XX
DR   WPI; 2004-011526/01.
XX
PT   Inspecting genetic susceptibility of Helicobacter pylori- related gastric
PT   carcinoma by checking Lewis blood-type antigen-associated gene
PT   polymorphism, applicable in screening individuals with high risk.
XX
PS   Example 2; Page 14; 37pp; Chinese.
XX
CC   The invention relates to a method for inspecting the genetic
CC   susceptibility of Helicobacter pylori related gastric carcinoma. The
CC   method of the invention comprises checking the polymorphism of the Lewis
CC   blood-type antigen-associated gene, with susceptibility particularly
CC   based on the recessive se allele and/or dominant homozygous Se/Se
CC   genotype. The method is applicable in screening individuals with high
CC   risk and in a follow-up survey for intervention, prevention and early
CC   diagnosis. In an experiment from the invention the Lewis gene fragments
CC   with T59G, G508A and T1067A polymorphism sites for PCR amplification were
CC   obtained for use after extracting samples of peripheral lymphocyte DNA
CC   from subjects. The mutation was then identified for assessing disease
CC   risk and diagnosis. The current sequene represents a PCR primer for
CC   amplification of a region of the Lewis gene.
XX
SQ   Sequence 18 BP; 4 A; 6 C; 6 G; 2 T; 0 U; 0 Other;

  Query Match             62.0%;  Score 12.4;  DB 12;  Length 18;
  Best Local Similarity   92.9%;  Pred. No. 3.3e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 ACTCTTGCAGGAAG 15
              ||||| ||||||||
Db          3 ACTCTGGCAGGAAG 16


RESULT 14
AAQ71136/c
ID   AAQ71136 standard; cDNA; 20 BP.
XX
AC   AAQ71136;
XX
DT   25-MAR-2003  (revised)
DT   20-APR-1995  (first entry)
XX
DE   Merlin exon 10 primer #1, amplifies 260 bp product.
XX
KW   Polymerase chain reaction; PCR; amplify; primer; bi-lateral schwannoma;
KW   sequence-tagged site assay; chromosome 22; NF2; deletion; hearing loss;
KW   neurofibromatosis; merlin; moesin-erzin-radixin-like protein; D22S28;
KW   tumour suppressor; activity; meningioma; cytoskeleton; gene therapy;
KW   merlin-associated tumour; D22S1; posterior capsular lens opacity;
KW   deafness; balance disorder; paralysis; ss.
XX
OS   Synthetic.
XX
PN   EP613945-A2.
XX
PD   07-SEP-1994.
XX
PF   25-FEB-1994;   94EP-00301367.
XX
PR   25-FEB-1993;   93US-00022034.
PR   04-MAR-1993;   93US-00026063.
PR   19-AUG-1993;   93US-00108808.
PR   22-DEC-1993;   93US-00171718.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Trofatter JA,  Maccollin MM,  Gusella JF;
XX
DR   WPI; 1994-272992/34.
XX
PT   The tumour suppressor gene merlin - for treatment and diagnosis of
PT   tumours and neurofibromatosis (NF2).
XX
PS   Example 6; Page 27; 86pp; English.
XX
CC   The sequences given in AAQ71110-55 are primers which were used to amplify
CC   the 17 exons of the NF2 gene. NF2 is a neurofibromatosis which is
CC   characterised by bi-lateral schwannomas. The NF2 "gene" has been shown by
CC   linkage studies to be assigned to chromosome 22. The missing or mutated
CC   gene in NF2 patients has been shown to be the merlin gene. The gene
CC   encodes a protein, merlin (moesin-erzin-radixin-like protein), which
CC   possesses tumour suppressor activity, and whose tumour suppressor
CC   activity is mediated by interactions with the cytoskeleton. The merlin
CC   gene is found on chromosome 22 between the known markers D22S1 and
CC   D22S28. In patients suffering from NF2, the merlin gene is either lost or
CC   mutated. A mutant merlin protein may be encoded by a gene in which a
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CC   mutation of A to T at the first position of the codon encoding amino acid
CC   220 causes the substitution of Tyr for Asn. The merlin gene may be used
CC   in gene therapy for the treatment of a merlin-associated tumour or NF2,
CC   or for prevention of schwannoma, meningioma, posterior capsular lens
CC   opacities, deafness or hearing loss, balance disorders or paralysis.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match            62.0%;  Score 12.4;  DB 2;  Length 20;
  Best Local Similarity  92.9%;  Pred. No. 3.3e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CTCTTGCAGGAAGC 16
              |||||||||| |||
Db         15 CTCTTGCAGGTAGC 2


RESULT 15
AAT90721/c
ID   AAT90721 standard; cDNA; 20 BP.
XX
AC   AAT90721;
XX
DT   12-FEB-1998  (first entry)
XX
DE   Human KVLQT1 S4 region PCR primer 5.
XX
KW   KVLQT1; long QT syndrome; arrhythmia; minK; potassium channel; diagnosis;
KW   therapy; human; single strand conformation polymorphism; primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9723598-A2.
XX
PD   03-JUL-1997.
XX
PF   20-DEC-1996;   96WO-US019756.
XX
PR   22-DEC-1995;   95US-0019014P.
PR   29-OCT-1996;   96US-00739383.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
XX
PI   Keating MT,  Sanguinetti MC,  Curran ME;
XX
DR   WPI; 1997-402190/37.
XX
PT   Human minK and Xenopus KVLQT1 coding sequences - used for assays for
PT   identifying drugs which can be used for preventing or treating long QT
PT   syndrome.
XX
PS   Example 12; Page 44; 105pp; English.
XX
CC   PCR primer 5 (AAT90721) and primer 6 (AAT90722) were designed to amplify
CC   DNA encoding the S4 region of human KVLQT1 (see AAW30038). PCR primers
CC   (AAT90717-28) were used in single-strand conformation analysis (SSCP) to
CC   define mutations in the human KVLQT1 gene (see AAT90730) associated with
CC   long QT syndrome (LQT). An initial SSCP identified an anomalous conformer
CC   in LQT-affected members of 6 large families. Further SSCP analyses
CC   identified a KVLQT1 intragenic deletion and 9 missense mutations
CC   associated with LQT in small families and sporadic cases
XX
SQ   Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;

  Query Match            62.0%;  Score 12.4;  DB 2;  Length 20;
  Best Local Similarity  92.9%;  Pred. No. 3.3e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 TGCAGGAAGCGGCT 20
              |||||||||||| |
Db         18 TGCAGGAAGCGGAT 5


RESULT 16
AAT91069/c
ID   AAT91069 standard; DNA; 20 BP.
XX
AC   AAT91069;
XX
DT   01-MAR-1998  (first entry)
XX
DE   Human KVLQT1 S4 region PCR primer 5.
XX
KW   KVLQT1; long QT syndrome; arrhythmia; minK; potassium channel; diagnosis;
KW   therapy; human; PCR; primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9723632-A1.
XX
PD   03-JUL-1997.
XX
PF   20-DEC-1996;   96WO-US019917.
XX
PR   22-DEC-1995;   95US-0019014P.
PR   29-OCT-1996;   96US-00739383.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
PA   (GENZ ) GENZYME GENETICS.
XX
PI   Keating MF,  Curran ME,  Landes GM,  Connors TD;
XX
DR   WPI; 1997-402191/37.
XX
PT   New isolated human potassium channel gene, KVLQT1, - used to develop
PT   products for diagnosis, prevention and therapy of long QT syndrome.
XX
PS   Example 12; Page 44; 105pp; English.
XX
CC   PCR primer 5 (AAT91069) and primer 6 (AAT91070) were designed to amplify
CC   DNA encoding the S4 region of human KVLQT1 (see AAW33355). PCR primers
CC   (AAT91065-76) were used in single-strand conformation analysis (SSCP) to
CC   define mutations in the human KVLQT1 gene (see AAT94004) associated with
CC   long QT syndrome (LQT). An initial SSCP identified an anomalous conformer
CC   in LQT-affected members of 6 large families. Further SSCP analyses
CC   identified a KVLQT1 intragenic deletion and 9 missense mutations
CC   associated with LQT in small families and sporadic cases
XX
SQ   Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;

  Query Match            62.0%;  Score 12.4;  DB 2;  Length 20;
  Best Local Similarity  92.9%;  Pred. No. 3.3e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 TGCAGGAAGCGGCT 20
              |||||||||||| |
Db         18 TGCAGGAAGCGGAT 5


RESULT 17
AAZ90745/c
ID   AAZ90745 standard; DNA; 20 BP.
XX
AC   AAZ90745;
XX
DT   19-JUN-2000  (first entry)
XX
DE   Human KVLQT1 mutation defining primer 5.
XX
KW   KVLQT1; KCNE1; long QT syndrome; LQT syndrome; minK protein;
KW   antiarrhythmic; gene therapy; human; PCR primer; ss.
XX
OS   Homo sapiens.
```

XX
PN WO200006600-A1.
XX
PD 10-FEB-2000.
XX
PF 06-OCT-1998; 98WO-US017838.
XX
PR 29-JUL-1998; 98US-0094477P.
PR 17-AUG-1998; 98US-00135020.
XX
PA (UTAH) UNIV UTAH RES FOUND.
XX
PI Keating MT, Sanguinetti MC, Splawski I;
XX
DR WPI; 2000-195262/17.
XX
PT Mutant forms of genes encoding minK protein and KVLQT1 protein involved
PT in cardiac potassium channel formation useful for screening drugs, for
PT preventing and treating cardiac arrhythmia.
XX
PS Example 13; Page 75; 167pp; English.
XX
CC The invention relates to KVLQT1 and KCNE1 genes, associated with long QT
CC (LQT) syndrome. It provides a minK protein comprising a mutation which
CC substitutes the wild type amino acids with Leu, Asp, Leu, His, Trp and
CC Ala or Thr at residues 74,76,28,32,98 and 127 respectively. Screening
CC KVLQT1 and KCNE1 is useful for identifying mutations for diagnosing and
CC treating LQT. The ability to predict LQT enables physicians to prevent
CC the diseases with medical therapy such as beta blocking agents and opts
CC for better treatments. Sequences AAZ90741-Z90752 represent PCR primers
CC for defining human KVLQT1 mutations
XX
SQ Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 62.0%; Score 12.4; DB 3; Length 20;
Best Local Similarity 92.9%; Pred. No. 3.3e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 TGCAGGAAGCGGCT 20
||||||||||||| |
Db 18 TGCAGGAAGCGGAT 5

RESULT 18
AAZ98975/c
ID AAZ98975 standard; DNA; 20 BP.
XX
AC AAZ98975;
XX
DT 06-JUN-2000 (first entry)
XX
DE Mutant human long QT syndrome-associated KVLQT1 diagnostic primer 5.
XX
KW KVLQT1; mutation; human; cardiac I(ks) potassium channel; KCNE1; ss;
KW cardiac arrhythmia; electrocardiogram; Long QT syndrome; gene therapy;
KW chromosome 11p15.5; PCR primer.
XX
OS Homo sapiens.
XX
PN WO200006199-A1.
XX
PD 10-FEB-2000.
XX
PF 12-MAY-1999; 99WO-US010260.
XX
PR 29-JUL-1998; 98US-0094477P.
PR 17-AUG-1998; 98US-00135010.
XX
PA (UTAH) UNIV UTAH RES FOUND.
PA (GENZ) GENZYME CORP.
XX
PI Keating MT, Sanguinetti MC, Curran ME, Landes GM, Connors TD;
PI Burn TC, Splawski I;
XX
DR WPI; 2000-195199/17.
XX
PT New isolated mutant KVLQT1 nucleic acids, useful for developing products
PT for the diagnosis, prevention and treatment of long QT syndrome.
XX
PS Example 13; Page 78; 178pp; English.
XX
CC The invention relates to KVLQT1 nucleic acids which have a mutation
CC compared to wild-type KVLQT1 (AAZ98901) The KVLQT1 gene encodes a protein
CC of 676 amino acids which forms a cardiac I(ks) potassium channel with the
CC KCNE1 protein (AAY80563). The KVLQT1 gene contains 15 introns and encodes
CC a protein containing 6 putative transmembrane segments and a pore forming
CC region. The gene has been mapped to the chromosomal location 11p15.5. The
CC sequences AAZ98971-Z98982 represent PCR primers used to diagnose
CC mutations in the KLVLQT1 gene. Mutations in the KVLQT1 or KCNE1 genes
CC result in cardiac arrhythmias observed as a prolonged QT curve in
CC electrocardiograms (Long QT syndrome). The genes and proteins can be used
CC for the diagnosis of subjects with long QT syndrome. They can also be
CC used to screen for drugs which can be used for treating or preventing
CC long QT syndrome. The KVLQT1 nucleic acids can be used for gene therapy,
CC and KVLQT1 peptides can be used for peptide therapy
XX
SQ Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 62.0%; Score 12.4; DB 3; Length 20;
Best Local Similarity 92.9%; Pred. No. 3.3e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 TGCAGGAAGCGGCT 20
||||||||||||| |
Db 18 TGCAGGAAGCGGAT 5

RESULT 19
ADR72365/c
ID ADR72365 standard; DNA; 20 BP.
XX
AC ADR72365;
XX
DT 02-DEC-2004 (first entry)
XX
DE Antisense oligo targeted to human kinesin-like 1, ISIS 344901.
XX
KW Antisense; kinesin-like 1; N2 kinesin; bimC kinesin;
KW cellular proliferation; cancer; B-cell leukaemia; autoimmune disease;
KW carpal tunnel syndrome; Raynaud's phenomenon; systemic sclerosis;
KW Sjorgren's syndrome; rheumatoid arthritis; polymyositis; polyarteritis;
KW systemic lupus erythematosus; human; ss; ISIS 344901; rat.
XX
OS Homo sapiens.
OS Rattus sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate nucleotide. All cytosines
FT are 5-methylcytidines. Residues 1 to 5 and 15 to 20 are
FT 2'-methoxyethyl nucleotides."
XX
PN US2004180847-A1.
XX
PD 16-SEP-2004.
XX
PF 17-NOV-2003; 2003US-00714796.
XX
PR 23-MAY-2002; 2002US-00156603.
XX
PA (DOBI/) DOBIE K W.
PA (KOLL/) KOLLER E.
XX

```
PI   Dobie KW,  Koller E;
XX
DR   WPI; 2004-652550/63.
XX
PT   New antisense compound 8 to 80 nucleobases in length targeted to a
PT   nucleic acid molecule encoding kinesin-like 1, useful for treating an
PT   animal having a disease or condition such as cancer, tumor, autoimmune
PT   disease.
XX
PS   Example 30; SEQ ID NO 129; 110pp; English.
XX
CC   The present invention relates to antisense compounds, compositions and
CC   methods for modulating the expression of kinesin-like 1. The superfamily
CC   of kinesins function as molecular engines to bind and transport vesicles
CC   and organelles along microtubules using energy supplied by ATP. Kinesin-
CC   like 1, a member of the N2 (also called bimC) family of kinesins, is
CC   involved in separating the chromosomes by directing their movement along
CC   microtubules in the bipolar spindle. Kinesin-like 1 is also known as
CC   KNSL1, Eg5, HsEg5, HKSP, KIF11, thyroid interacting protein 5 and TRIP5.
CC   Inhibition of kinesin-like 1 may be a target for arresting cellular
CC   proliferation in cancer, due to its central role in mitosis. Expression
CC   of kinesin-like 1 expression may contribute to other disease states such
CC   as B-cell leukaemia, autoimmune diseases such as carpal tunnel syndrome,
CC   Raynaud's phenomenon, systemic sclerosis, Sjorgren's syndrome, rheumatoid
CC   arthritis, polymyositis and polyarteritis. Kinesin-like 1 is an
CC   autoantigen identified in systemic lupus erythematosus. The invention
CC   relates to antisense nucleic acid oligomers, targeted to the gene
CC   encoding kinesin-like 1. Also provided are methods of screening for
CC   modulators of kinesin-like 1 and to methods of modulating the expression
CC   of kinesin-like 1. At least a portion of the compound hybridises with RNA
CC   to form an oligonucleotide-RNA duplex. It has at least one modified
CC   internucleoside linkage, sugar moiety, or nucleobase. It has at least one
CC   2'-O-methoxyethyl sugar moiety, phosphorothioate internucleoside linkage,
CC   or one cytosine which is a 5-methylcytosine. The antisense compound may
CC   comprise an antisense nucleic acid molecule that is specifically
CC   hybridisable with a 5'-untranslated region (UTR), with a start region,
CC   with a coding region, with a 3'-UTR, with an intron, or with an intron-
CC   exon junction of a nucleic acid molecule encoding kinesin-like 1.
CC   Oligonucleotides were synthesised via solid phase P(III) phosphoramidite
CC   chemistry. The present sequence is an antisense oligo targeted to human
CC   kinesin-like 1, ISIS #344902.
XX
SQ   Sequence 20 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 0 Other;

  Query Match             62.0%;  Score 12.4;  DB 13;  Length 20;
  Best Local Similarity   92.9%;  Pred. No. 3.3e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TCTTGCAGGAAGCG 17
              ||||||||||||| |
Db         20 TCTTGCAGGAAGTG 7


RESULT 20
ADR72397/c
ID   ADR72397 standard; DNA; 20 BP.
XX
AC   ADR72397;
XX
DT   02-DEC-2004  (first entry)
XX
DE   Antisense oligo targeted to mouse kinesin-like 1, ISIS 285690.
XX
KW   Antisense; kinesin-like 1; N2 kinesin; bimC kinesin;
KW   cellular proliferation; cancer; B-cell leukaemia; autoimmune disease;
KW   carpal tunnel syndrome; Raynaud's phenomenon; systemic sclerosis;
KW   Sjorgren's syndrome; rheumatoid arthritis; polymyositis; polyarteritis;
KW   systemic lupus erythematosus; mouse; ss; human.
XX
OS   Mus musculus.
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= phosphorothioate nucleotide. All cytosines
FT                   are 5-methylcytidines. Residues 1 to 5 and 15 to 20 are
FT                   2'-methoxyethyl nucleotides."
XX
PN   US2004180847-A1.
XX
PD   16-SEP-2004.
XX
PF   17-NOV-2003; 2003US-00714796.
XX
PR   23-MAY-2002; 2002US-00156603.
XX
PA   (DOBI/) DOBIE K W.
PA   (KOLL/) KOLLER E.
XX
PI   Dobie KW,  Koller E;
XX
DR   WPI; 2004-652550/63.
XX
PT   New antisense compound 8 to 80 nucleobases in length targeted to a
PT   nucleic acid molecule encoding kinesin-like 1, useful for treating an
PT   animal having a disease or condition such as cancer, tumor, autoimmune
PT   disease.
XX
PS   Claim 36; SEQ ID NO 161; 110pp; English.
XX
CC   The present invention relates to antisense compounds, compositions and
CC   methods for modulating the expression of kinesin-like 1. The superfamily
CC   of kinesins function as molecular engines to bind and transport vesicles
CC   and organelles along microtubules using energy supplied by ATP. Kinesin-
CC   like 1, a member of the N2 (also called bimC) family of kinesins, is
CC   involved in separating the chromosomes by directing their movement along
CC   microtubules in the bipolar spindle. Kinesin-like 1 is also known as
CC   KNSL1, Eg5, HsEg5, HKSP, KIF11, thyroid interacting protein 5 and TRIP5.
CC   Inhibition of kinesin-like 1 may be a target for arresting cellular
CC   proliferation in cancer, due to its central role in mitosis. Expression
CC   of kinesin-like 1 expression may contribute to other disease states such
CC   as B-cell leukaemia, autoimmune diseases such as carpal tunnel syndrome,
CC   Raynaud's phenomenon, systemic sclerosis, Sjorgren's syndrome, rheumatoid
CC   arthritis, polymyositis and polyarteritis. Kinesin-like 1 is an
CC   autoantigen identified in systemic lupus erythematosus. The invention
CC   relates to antisense nucleic acid oligomers, targeted to the gene
CC   encoding kinesin-like 1. Also provided are methods of screening for
CC   modulators of kinesin-like 1 and to methods of modulating the expression
CC   of kinesin-like 1. At least a portion of the compound hybridises with RNA
CC   to form an oligonucleotide-RNA duplex. It has at least one modified
CC   internucleoside linkage, sugar moiety, or nucleobase. It has at least one
CC   2'-O-methoxyethyl sugar moiety, phosphorothioate internucleoside linkage,
CC   or one cytosine which is a 5-methylcytosine. The antisense compound may
CC   comprise an antisense nucleic acid molecule that is specifically
CC   hybridisable with a 5'-untranslated region (UTR), with a start region,
CC   with a coding region, with a 3'-UTR, with an intron, or with an intron-
CC   exon junction of a nucleic acid molecule encoding kinesin-like 1.
CC   Oligonucleotides were synthesised via solid phase P(III) phosphoramidite
CC   chemistry. The present sequence is an antisense oligo targeted to mouse
CC   kinesin-like 1.
XX
SQ   Sequence 20 BP; 5 A; 5 C; 2 G; 8 T; 0 U; 0 Other;

  Query Match             62.0%;  Score 12.4;  DB 13;  Length 20;
  Best Local Similarity   92.9%;  Pred. No. 3.3e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TCTTGCAGGAAGCG 17
              ||||||||||||| |
Db         19 TCTTGCAGGAAGTG 6


RESULT 21
```

ABN08122
ID ABN08122 standard; DNA; 17 BP.
XX
AC ABN08122;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8114.
XX
KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
PN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
DR WPI; 2002-179446/23.
XX
PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
PS Disclosure; SEQ ID NO 8114; 214pp; English.
XX
CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 3 A; 6 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 61.0%; Score 12.2; DB 6; Length 17;
Best Local Similarity 82.4%; Pred. No. 4.1e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          4 TCTTGCAGGAAGCGGCT 20
              || |||  |||||||||
Db          1 TCCTGCCAGAAGCGGCT 17
```

RESULT 22
ACN71212
ID ACN71212 standard; DNA; 17 BP.
XX
AC ACN71212;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human GDMLP-1 probe SEQ ID NO:8114.
XX
KW Human; ss; probe; myosin-like protein-1; hGDMLP-1;
KW hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
KW skeletal muscle function.
XX
OS Homo sapiens.
XX
PN US2004137589-A1.
XX
PD 15-JUL-2004.
XX
PF 26-NOV-2003; 2003US-00723361.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
PR 25-MAY-2001; 2001US-00866108.
XX
PA (GUYY/) GU Y.
PA (JIYY/) JI Y.
PA (PENN/) PENN S G.
PA (HANZ/) HANZEL D K.
PA (RANK/) RANK D.
PA (CHEN/) CHEN W.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
XX
DR WPI; 2004-533378/51.
XX
PT Novel myosin-like protein-1, useful for treating or preventing disorder
PT associated with decreased expression or activity of human genome-derived
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
PT function.
XX
PS Disclosure; SEQ ID NO 8114; 0pp; English.
XX
CC The invention relates to a novel polypeptide (I) comprising a sequence
CC (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully
CC defined in the specification, a fragment of at least 8 amino acids of
CC (S1), 95% deviation from (S1) which are conservative substitutions, and
CC 65% identity to (S1). A polypeptide of the invention acts as a agonist or

```
CC   antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A
CC   pharmaceutical composition of the invention is useful for treating or
CC   preventing a disorder associated with decreased expression or activity of
CC   hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.
CC   The present sequence represents a 17-mer nucleotide, used in the
CC   invention for scanning the sequence represented in ACN63103
XX
SQ   Sequence 17 BP; 3 A; 6 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             61.0%;  Score 12.2;  DB 13;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 4.1e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 TCTTGCAGGAAGCGGCT 20
              || |||  |||||||||
Db          1 TCCTGCCAGAAGCGGCT 17


RESULT 23
AAC67455/c
ID   AAC67455 standard; DNA; 18 BP.
XX
AC   AAC67455;
XX
DT   14-FEB-2001  (first entry)
XX
DE   Alzheimer's disease-linked mitochondrial SNP PCR primer #155.
XX
KW   Human; mitochondrial genome; single nucleotide polymorphism; SNP;
KW   Alzheimer's disease; mtDNA; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200063441-A2.
XX
PD   26-OCT-2000.
XX
PF   19-APR-2000; 2000WO-US010906.
XX
PR   20-APR-1999;   99US-0130447P.
PR   22-OCT-1999;   99US-0160901P.
XX
PA   (MITO-) MITOKOR.
XX
PI   Herrnstadt C,  Davis RE;
XX
DR   WPI; 2000-672748/65.
XX
PT   Diagnosing a subject at the risk for or having Alzheimer's disease
PT   comprises determining at least one single nucleotide polymorphism in
PT   mitochondrial DNA associated with the disease in the sample from the
PT   subject.
XX
PS   Example 4; Page 41; 89pp; English.
XX
CC   The present invention describes a novel method for determining the risk
CC   of or diagnosing Alzheimer's disease using single nucleotide
CC   polymorphisms (SNPs) present in an individual's mitochondrial DNA
CC   (mtDNA). In additon, the SNPs identified can be used to identify agents
CC   suitable for use in treating Alzheimer's disease. Sequences AAC67301-
CC   C67610 are PCR primers used to demonstrate the method of the invention
XX
SQ   Sequence 18 BP; 5 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             61.0%;  Score 12.2;  DB 3;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 4.1e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 ACTCTTGCAGGAAGCGG 18
              | ||||||| ||| |||
Db         17 ATTCTTGCACGAAACGG 1


RESULT 24
AAA83794/c
ID   AAA83794 standard; DNA; 19 BP.
XX
AC   AAA83794;
XX
DT   04-DEC-2000  (first entry)
XX
DE   cdk-we-hu ribozyme binding site #269.
XX
KW   Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX
OS   Mammalia.
XX
PN   WO200032765-A2.
XX
PD   08-JUN-2000.
XX
PF   06-DEC-1999;   99WO-US028772.
XX
PR   04-DEC-1998;   98US-0110954P.
XX
PA   (IMMU-) IMMUSOL INC.
XX
PI   Tritz R,  Welch PJ,  Barber JR,  Robbins JM;
XX
DR   WPI; 2000-412314/35.
XX
PT   New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT   RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT   PCNA and Cyclin B1.
XX
PS   Disclosure; Page 67; 109pp; English.
XX
CC   The present invention relates to a hairpin or hammerhead ribozyme,
CC   designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC   other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC   Representative examples of ribozyme recognition sites are given in
CC   AAA82415 to AAA86787. The ribozyme of the invention is useful for
CC   inhibiting restenosis by introduction of the ribozyme into cells. The
CC   ribozyme is resistant to endonuclease activity and hence is efficient in
CC   restenosis treatment
XX
SQ   Sequence 19 BP; 5 A; 4 C; 5 G; 5 T; 0 U; 0 Other;

  Query Match             61.0%;  Score 12.2;  DB 3;  Length 19;
  Best Local Similarity   82.4%;  Pred. No. 4.1e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 ACTCTTGCAGGAAGCGG 18
              |||||| |  |||||||
Db         18 ACTCTTTCTAGAAGCGG 2


RESULT 25
AAH58956/c
ID   AAH58956 standard; DNA; 19 BP.
XX
AC   AAH58956;
XX
DT   10-SEP-2001  (first entry)
XX
DE   Cdk-we-hu ribozyme binding site SEQ ID NO:1380.
XX
KW   Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW   recognition site; target; ribozyme binding site; eye disease; vulnerary;
KW   proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW   cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW   matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW   antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW   antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
KW   atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW   basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
```

KW sickle cell retinopathy; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200130362-A2.
XX
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-US029500.
XX
PR 26-OCT-1999; 99US-0161532P.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Robbins JM, Tritz R;
XX
DR WPI; 2001-300427/31.
XX
PT Treating proliferative skin or eye diseases and scarring, using ribozymes
PT that cleave RNA encoding cytokines involved in inflammation, matrix
PT metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
PS Example 1; Page 172; 408pp; English.
XX
CC The present invention describes a method for treating a proliferative
CC skin or eye disease and scarring. The method involves administering a
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC dependent kinase, growth factor or a reductase, or administering a
CC nucleic acid molecule (II) comprising a promoter operably linked to a
CC nucleic acid segment encoding (I). (I) can have antipsoriatic,
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
CC ophthalmological, vulnerary, keratolytic and virucide activities, and
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC in gene therapy. (I) and (II) are useful for treating proliferative skin
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 19 BP; 5 A; 4 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 61.0%; Score 12.2; DB 5; Length 19;
Best Local Similarity 82.4%; Pred. No. 4.1e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ACTCTTGCAGGAAGCGG 18
|||||| | |||||||
Db 18 ACTCTTTCTAGAAGCGG 2

RESULT 26
ADT01798
ID ADT01798 standard; DNA; 19 BP.
XX
AC ADT01798;
XX
DT 16-DEC-2004 (first entry)
XX
DE Novel mutant protein tyrosine kinase-related oligonucleotide SeqID1786.
XX
KW tyrosine kinase; cancer; anti-cancer agent; signalling molecule;
KW tumourigenesis; somatic alteration; colorectal cancer; NTRK3; FES;
KW GUCY2F; MCCK; MLK4; kinase domain; cytostatic; tyrosine kinase inhibitor;
KW guanylate cyclase stimulator; ss.
XX
OS Homo sapiens.
XX
PN WO2004082458-A2.
XX
PD 30-SEP-2004.
XX
PF 18-FEB-2004; 2004WO-US004452.
XX
PR 21-FEB-2003; 2003US-0448537P.
PR 29-MAY-2003; 2003US-0473895P.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Bardelli A, Parsons W, Velculescu V, Kinzler KW, Vogelstein B;
XX
DR WPI; 2004-718702/70.
XX
PT Activated mutant protein tyrosine kinases (e.g. NTRK3, FES and MCCK) and
PT associated methods for diagnosing cancer and screening for anti-cancer
PT agents.
XX
PS Disclosure; SEQ ID NO 1786; 363pp; English.
XX
CC This invention relates to a novel activated mutant protein tyrosine
CC kinases and associated methods for diagnosing cancer and screening for
CC anti-cancer agents. Protein kinases are signalling molecules involved in
CC tumourigenesis. Mutational analysis of the human tyrosine kinase gene
CC family identified somatic alteration sin 1 in 5 colorectal cancers, with
CC the majority of mutations occurring in the NTRK3, FES, GUCY2F and
CC MCCK/MLK4 genes. Most were identified in the kinase domain. The invention
CC may be useful for the production of compounds with a cytostatic activity
CC acting as protein tyrosine kinase inhibitors or guanylate cyclase
CC stimulators. The invention may be useful for developing methods for
CC detecting mutations involved in cancer or screening for anti-cancer
CC agents. The present sequence is that of a human-derived oligonucleotide
CC which is related to the invention.
XX
SQ Sequence 19 BP; 6 A; 4 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 61.0%; Score 12.2; DB 13; Length 19;
Best Local Similarity 82.4%; Pred. No. 4.1e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAAGCG 17
|||| |||||||| ||
Db 3 GACTGCTGCAGGAAACG 19

RESULT 27
AAT89003/c
ID AAT89003 standard; DNA; 20 BP.
XX
AC AAT89003;
XX
DT 22-APR-1998 (first entry)
XX
DE Human maspin Ets wild-type sense oligonucleotide DNA.
XX
KW Maspin; serpin; mammary epithelial cell; human; promoter; malignant;
KW tumour cell; treatment; prostate cancer; breast cancer; metastasis;
KW primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9736179-A1.
XX
PD 02-OCT-1997.
XX
PF 28-MAR-1997; 97WO-US005186.
XX
PR 28-MAR-1996; 96US-0014368P.
XX
PA (DAND) DANA FARBER CANCER INST.
PA (PARD/) PARDEE A.

```
XX
PI   Sagar R,  Zhang M;
XX
DR   WPI; 1997-489785/45.
XX
PT   Maspin gene promoter fragment - used to identify compounds for treatment
PT   of prostate or breast cancer.
XX
PS   Disclosure; Page 12; 51pp; English.
XX
CC   Primers AAT89003-T89008 are used in electrophoretic mobility shift assay
CC   experiments to analyse the maspin promoter region. AAT89003 is designed
CC   as a Ets regulatory element wild type (WT) sense oligonucleotide. Maspin
CC   is a serpin which is expressed in mammary epithelial cells. Its
CC   expression in these cells decreases with increasing malignancy and is
CC   lost in during metastasis. Maspin protein is also known to inhibit the
CC   mobility of tumour cells. This gene can be used in method for screening
CC   compounds to identify candidate compounds for the treatment of prostate
CC   cancer, or breast cancer. It can also be used to identify compounds that
CC   increase the expression of maspin, and for detecting the presence of
CC   metastatic prostate epithelial cells
XX
SQ   Sequence 20 BP; 3 A; 11 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             61.0%;  Score 12.2;  DB 2;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 4.1e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 TCTTGCAGGAAGCGGCT 20
              ||  |||||||| ||||
Db         18 TCGGGCAGGAAGGGGCT 2


RESULT 28
AAZ02042
ID   AAZ02042 standard; DNA; 20 BP.
XX
AC   AAZ02042;
XX
DT   07-OCT-1999  (first entry)
XX
DE   PCR primer used to amplify an ORF of Chlamydia trachomatis.
XX
KW   Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
KW   paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
KW   nongonococcal uretritis; epidymitis; cervicitis; salpingitis; PCR primer;
KW   bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
XX
OS   Synthetic.
OS   Chlamydia trachomatis.
XX
PN   WO9928475-A2.
XX
PD   10-JUN-1999.
XX
PF   27-NOV-1998;   98WO-IB001939.
XX
PR   28-NOV-1997;   97FR-00015041.
PR   17-DEC-1997;   97FR-00016034.
PR   04-NOV-1998;   98US-0107077P.
XX
PA   (GEST ) GENSET.
XX
PI   Griffais R;
XX
DR   WPI; 1999-371125/31.
XX
PT   Genome sequence of Chlamydia trachomatis.
XX
PS   Disclosure; Page 1492; 1755pp; English.
XX
CC   PCR primers AAZ01426-Z06209 were used to amplify open reading frames
CC   (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
CC   encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
CC   against Chlamydia trachomatis. Antisense and ribozyme sequences can also
CC   be used to control growth of the microorganism. Chlamydia trachomatis is
CC   responsible for a large number of diseases, e.g. eye diseases such as
CC   conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion
CC   conjunctivitis; genital diseases such as nongonococcal uretritis,
CC   epidymitis, cervicitis, salpingitis, perihepatitis, bartholinitis;
CC   pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
CC   The polypeptides of the invention may be of use in treating these
CC   diseases
XX
SQ   Sequence 20 BP; 4 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

  Query Match             61.0%;  Score 12.2;  DB 2;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 4.1e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GACTCTTGCAGGAAGCG 17
              |||||||| ||||  ||
Db          4 GACTCTTGAAGGACTCG 20


RESULT 29
AAX79782/c
ID   AAX79782 standard; DNA; 20 BP.
XX
AC   AAX79782;
XX
DT   17-AUG-1999  (first entry)
XX
DE   PCR primer H15340 for mitochondrial DNA analysis.
XX
KW   PCR primer; human; mitochondrial DNA; genetic diagnosis;
KW   adult disease contraction; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   JP11113597-A.
XX
PD   27-APR-1999.
XX
PF   13-OCT-1997;   97JP-00279127.
XX
PR   13-OCT-1997;   97JP-00279127.
XX
PA   (TANA/) TANAKA M.
XX
DR   WPI; 1999-320841/27.
XX
PT   Genetic diagnosis using human mitochondrial DNA - comprises detecting
PT   base replacements.
XX
PS   Example 2; Page 6; 15pp; Japanese.
XX
CC   This sequence represents a PCR primer that can be used in the method of
CC   the invention. The method is for genetic diagnosis using human
CC   mitochondrial DNA where there is at least one base replacement from among
CC   the following five replacements: the 3010th base is changed from guanine
CC   to adenine; the 4883rd base from cytosine to thymine; the 5178th base
CC   from cytosine to adenine; the 8414th base from cytosine to thymine; and
CC   the 14668th base from cytosine to thymine. The method can be used for
CC   diagnosing the probability of contracting adult diseases. A confirmation
CC   of base replacement can give a diagnosis of the level of probability of
CC   contraction of adult diseases
XX
SQ   Sequence 20 BP; 5 A; 5 C; 4 G; 6 T; 0 U; 0 Other;

  Query Match             61.0%;  Score 12.2;  DB 2;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 4.1e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 ACTCTTGCAGGAAGCGG 18
```

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              | ||||||| ||| |||
Db         20 ATTCTTGCACGAAACGG 4
```

RESULT 30
ACC70917/c
ID ACC70917 standard; DNA; 20 BP.
XX
AC ACC70917;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human cytochrome b PCR primer #10.
XX
KW Human; mitochondrial; Parkinson's disease; cytochrome b; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO2003033737-A1.
XX
PD 24-APR-2003.
XX
PF 15-OCT-2002; 2002WO-JP010640.
XX
PR 17-OCT-2001; 2001JP-00318805.
XX
PA (GIFU-) GIFU INT INST BIOTECHNOLOGY.
XX
PI Tanaka M;
XX
DR WPI; 2003-393541/37.
XX
PT Gene detection method using human mitochondrial DNA to reveal and confirm
PT amino acid substitution advantageous or disadvantageous in prolonged
PT survival of human, useful for diagnosis of Parkinson's disease.
XX
PS Disclosure; Page 7; 35pp; Japanese.
XX
CC The present invention relates to a detection method using human
CC mitochondrial (mt) DNA. The method comprises detecting the replacement of
CC a base accompanying an amino acid substitution in a protein encoded by
CC its base sequence in a human mitochondrial DNA base sequence. The method
CC is useful for diagnosis of Parkinson's disease, and in health checks and
CC assessing risks for other adult diseases. The present sequence is a PCR
CC primer, which was used to illustrate the invention
XX
SQ Sequence 20 BP; 5 A; 5 C; 4 G; 6 T; 0 U; 0 Other;

```
  Query Match             61.0%;  Score 12.2;  DB 8;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 4.1e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 ACTCTTGCAGGAAGCGG 18
              | ||||||| ||| |||
Db         20 ATTCTTGCACGAAACGG 4
```

RESULT 31
ADM14320/c
ID ADM14320 standard; DNA; 20 BP.
XX
AC ADM14320;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:507.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key   Location/Qualifiers
FT modified_base   1. .20
FT   /*tag= b
FT   /mod_base= OTHER
FT   /note= "phosphorothioate linkages and all cytidine
FT   residues are 5-methylcytidines"
FT modified_base   1. .5
FT   /*tag= a
FT   /mod_base= OTHER
FT   /note= "2'-O-methocyethyls"
FT modified_base   16. .20
FT   /*tag= c
FT   /mod_base= OTHER
FT   /note= "2'-O-methoxyethyls"
XX
PN WO2004028458-A2.
XX
PD 08-APR-2004.
XX
PF 25-SEP-2003; 2003WO-US030374.
XX
PR 25-SEP-2002; 2002US-0413549P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Gierse JK;
XX
DR WPI; 2004-305094/28.
XX
PT New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischemia.
XX
PS Claim 4; SEQ ID NO 507; 132pp; English.
XX
CC The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC human mPGES-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGES-1. MPGES-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antidiabetic, immunomodulator, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

```
  Query Match             61.0%;  Score 12.2;  DB 12;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 4.1e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 TCTTGCAGGAAGCGGCT 20
              || |||| |||| ||||
Db         20 TCCTGCACGAAGTGGCT 4
```

```
RESULT 32
ADM14505/c
ID   ADM14505 standard; DNA; 20 BP.
XX
AC   ADM14505;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:692.
XX
KW   chimeric; antisense oligonucleotide; phosphorothioate; human;
KW   microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW   microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic;
KW   immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW   neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW   immunomodulatory; cardiovascular; gene therapy; inflammation;
KW   Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW   reperfusion injury; ophthalmic disorder; immunological disorder;
KW   cardiovascular disorder; neurological disorder; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages and all cytidine
FT                   residues are 5-methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methocyethyls"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyls"
XX
PN   WO2004028458-A2.
XX
PD   08-APR-2004.
XX
PF   25-SEP-2003; 2003WO-US030374.
XX
PR   25-SEP-2002; 2002US-0413549P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Gierse JK;
XX
DR   WPI; 2004-305094/28.
XX
PT   New antisense compound, having a sequence targeted to a nucleic acid
PT   encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT   inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT   ischemia.
XX
PS   Claim 4; SEQ ID NO 692; 132pp; English.
XX
CC   The present sequence represents a chimeric antisense oligonucleotide
CC   targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC   human mPGES-1 gene is located on chromosome 9, more specifically to
CC   9q34.3. The present invention also describes: (1) antisense compounds,
CC   having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC   mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC   inhibits its expression; (2) a method of inhibiting the expression of
CC   mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC   having a disease or condition associated with mPGES-1. MPGES-1 chimeric
CC   antisense oligonucleotides and antisense compounds have cytostatic,
CC   antidiabetic, immunomodulator, cardiant, neuroprotective,
CC   antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC   ophthalmological, immunomodulatory and cardiovascular activities, and can
CC   be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC   can be used for preparing a composition for treating a disease or
CC   condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC   disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC   ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ   Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             61.0%;  Score 12.2;  DB 12;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 4.1e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 TCTTGCAGGAAGCGGCT 20
              || |||| |||| ||||
Db         19 TCCTGCACGAAGTGGCT 3


RESULT 33
AAF46592/c
ID   AAF46592 standard; DNA; 15 BP.
XX
AC   AAF46592;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGFBP3 oligonucleotide #12.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 7; Page 44; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
```

```
XX
SQ   Sequence 15 BP; 0 A; 7 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match            60.0%;  Score 12;  DB 4;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 5.1e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 GCAGGAAGCGGC 19
              ||||||||||||
Db         12 GCAGGAAGCGGC 1


RESULT 34
AAF46588/c
ID   AAF46588 standard; DNA; 15 BP.
XX
AC   AAF46588;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGFBP3 oligonucleotide #8.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 7; Page 44; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 1 A; 8 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match            60.0%;  Score 12;  DB 4;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 5.1e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 CAGGAAGCGGCT 20
              ||||||||||||
Db         15 CAGGAAGCGGCT 4


RESULT 35
ABT34760/c
ID   ABT34760 standard; DNA; 17 BP.
XX
AC   ABT34760;
XX
DT   12-JUN-2003  (first entry)
XX
DE   Tumour suppression related human fukutin oligo SEQ ID No 397.
XX
KW   Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW   antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW   schizophrenia; protein chip; gene therapy; tumour suppression;
KW   human fukutin; ds.
XX
OS   Homo sapiens.
XX
PN   WO2003025175-A2.
XX
PD   27-MAR-2003.
XX
PF   17-SEP-2002; 2002WO-IB004208.
XX
PR   17-SEP-2001; 2001FR-00011978.
XX
PA   (MOLE-) MOLECULAR ENGINES LAB.
XX
PI   Telerman A,  Amson R,  Tuijnder M;
XX
DR   WPI; 2003-313353/30.
XX
PT   New isolated nucleic acid, useful for treating viral diseases associated
PT   with tumors and cell degeneration, also related polypeptides, antibodies
PT   and transfected cells.
XX
PS   Disclosure; Page 80; 720pp; French.
XX
CC   The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC   given in the specification, a sequence containing at least 15 consecutive
CC   nucleotides from the 17 mer sequence, a sequence with, after optimal
CC   alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC   hybridizes to them under highly stringent conditions, or the complement
CC   of any of them, or the corresponding RNA. The novel isolated nucleic
CC   acids of the invention are useful as probes and primers for detecting,
CC   identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC   component of a gene chip, in vitro as (anti)sense reagents, and for
CC   production of recombinant polypeptides. Any of the nucleic acids,
CC   polypeptides, vectors containing the nucleic acids, cells containing the
CC   vector or antibodies directed against the polypeptides are useful for
CC   preparation of pharmaceuticals for prevention and/or treatment of viral
CC   diseases that are characterised by development of tumours or cell
CC   degeneration, specifically cancer but also Alzheimer's disease and
CC   schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC   patient samples is useful for diagnosis and/or prognosis of these
CC   diseases. The polypeptides can also be used to generate antibodies, and
CC   both the polypeptide and antibodies are useful as components of protein
CC   chips. The nucleic acid sequences of the invention can be used in gene
CC   therapy. This polynucleotide sequence represents a tumour suppression
CC   related human fukutin oligonucleotide of the invention
XX
SQ   Sequence 17 BP; 6 A; 3 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match            60.0%;  Score 12;  DB 8;  Length 17;
  Best Local Similarity  100.0%;  Pred. No. 5.1e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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```
Qy          2 ACTCTTGCAGGA 13
              ||||||||||||
Db         14 ACTCTTGCAGGA 3
```

RESULT 36
ACC54373
ID ACC54373 standard; DNA; 17 BP.
XX
AC ACC54373;
XX
DT 27-JUN-2003 (first entry)
XX
DE Human tumour suppressor sequence #3140.
XX
KW ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
KW tumour regression; apoptosis; virus resistance; diagnosis;
KW cellular degeneration.
XX
OS Homo sapiens.
XX
PN FR2826373-A1.
XX
PD 27-DEC-2002.
XX
PF 20-JUN-2001; 2001FR-00008139.
XX
PR 20-JUN-2001; 2001FR-00008139.
XX
PA (MOLE-) MOLECULAR ENGINES LAB SA.
XX
PI Tuijnder M, Telerman A, Amson R;
XX
DR WPI; 2003-250498/25.
XX
PT New nucleic acid sequences associated with tumor suppression, regression,
PT apoptosis or virus resistance are useful to diagnose and treat viral
PT disease, development of tumor cells and cell degeneration.
XX
PS Claim 1; Page 765; 798pp; French.
XX
CC This sequence represents an isolated nucleic acid sequence associated
CC with tumour suppression or regression, apoptosis or virus resistance. The
CC invention relates to these sequences or sequences having at least 80%
CC identity to them, and polypeptides encoded by the sequences or
CC polypeptides having 80% identity to the polypeptide sequences. The
CC invention is used to diagnose or treat viral disease or disease
CC characterized by development of tumour cells or cellular degeneration
XX
SQ Sequence 17 BP; 5 A; 2 C; 5 G; 5 T; 0 U; 0 Other;

  Query Match   60.0%; Score 12; DB 10; Length 17;
  Best Local Similarity   100.0%; Pred. No. 5.1e+04;
  Matches   12; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy          4 TCTTGCAGGAAG 15
              ||||||||||||
Db          3 TCTTGCAGGAAG 14
```

RESULT 37
ADF87984/c
ID ADF87984 standard; DNA; 19 BP.
XX
AC ADF87984;
XX
DT 26-FEB-2004 (first entry)
XX
DE Single nucleotide polymorphism detection primer, SEQ ID No 1567.
XX
KW human; single nucleotide polymorphism; microarray; side effect; ss;
KW primer; PCR.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN JP2003235571-A.
XX
PD 26-AUG-2003.
XX
PF 12-FEB-2002; 2002JP-00034717.
XX
PR 12-FEB-2002; 2002JP-00034717.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR WPI; 2003-820454/77.
XX
PT Novel polynucleotide useful for detecting single nucleotide polymorphisms
PT in human gene.
XX
PS Claim 2; SEQ ID NO 1567; 704pp; Japanese.
XX
CC The invention relates to a novel polynucleotide isolated and purified
CC from a human gene having any one of 935 fully defined sequences as given
CC in specification, or a sequence having a base substitution. The invention
CC further relates to: an oligonucleotide containing single nucleotide
CC polymorphisms; a PCR primer set chosen from the combination of two DNA
CC fragments from any one of 1220 fully defined sequences as given in
CC specification; a labelling probe containing the SNP containing oligo; and
CC a microarray equipped with the SNP containing oligo. The isolated human
CC gene of the invention is useful for detecting the single nucleotide
CC polymorphisms in human gene. The isolated human gene is also useful for
CC diagnosis of disease and determination of side effect to a medical agent.
CC The isolated human gene is also effective in detecting single nucleotide
CC polymorphisms in a human gene. This polynucleotide sequence represents
CC one of the PCR primers used in the single nucleotide polymorphism
CC detection method of the invention.
XX
SQ Sequence 19 BP; 1 A; 6 C; 5 G; 7 T; 0 U; 0 Other;

  Query Match   60.0%; Score 12; DB 10; Length 19;
  Best Local Similarity   100.0%; Pred. No. 5.2e+04;
  Matches   12; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy          9 CAGGAAGCGGCT 20
              ||||||||||||
Db         17 CAGGAAGCGGCT 6
```

RESULT 38
AAZ74144/c
ID AAZ74144 standard; DNA; 20 BP.
XX
AC AAZ74144;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker downstream amplification primer SEQ ID NO:8500.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB000822.
XX
PR 21-APR-1998; 98US-0082614P.

```
PR   23-NOV-1998;   98US-0109732P.
XX
PA   (GEST ) GENSET.
XX
PI   Cohen D,  Blumenfeld M,  Chumakov I;
XX
DR   WPI; 2000-013267/01.
XX
PT   Novel biallelic markers used to construct a high density disequilibrium
PT   map of the human genome.
XX
PS   Claim 8; Page 2043; 2745pp; English.
XX
CC   AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC   invention, which contain a polymorphic base at position 24 of their
CC   nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC   primers for the biallelic markers. The biallelic markers of the invention
CC   have a variety of uses: they can be used for high density mapping of the
CC   human genome, and in complex association studies and haplotyping studies
CC   which are useful in determining the genetic basis for disease states.
CC   Compositions and methods of the invention can also be useful for the
CC   identification of the targets for the development of pharmaceutical
CC   agents and diagnostic methods, as well as the characterisation of the
CC   differential efficacious responses to and side effects from
CC   pharmaceutical agents acting on a disease as well as other treatment.
CC   N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC   3367, are not actually given a sequence in the Sequence Listing from the
CC   present invention
XX
SQ   Sequence 20 BP; 6 A; 4 C; 4 G; 6 T; 0 U; 0 Other;

  Query Match             60.0%;  Score 12;  DB 3;  Length 20;
  Best Local Similarity   75.0%;  Pred. No. 5.2e+04;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GACTCTTGCAGGAAGCGGCT 20
              |||| |||||  |||| | |
Db         20 GACTTTTGCACTAAGCAGAT 1


RESULT 39
ABA02533
ID   ABA02533 standard; DNA; 16 BP.
XX
AC   ABA02533;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Lipoprotein lipase precursor SNP-5 reverse PCR primer.
XX
KW   Single-nucleotide polymorphism; SNP; diabetes; thalassaemia;
KW   sickle-cell anaemia; cystic fibrosis; oncogenic mutation; pathogen;
KW   paternity; prenatal testing; forensic investigation; genotyping;
KW   3'-5'-exonuclease; point mutation; lipoprotein lipase precursor; LPL;
KW   PCR; primer; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "6-carboxy-x-rhodamine (ROX)"
XX
PN   WO200181631-A1.
XX
PD   01-NOV-2001.
XX
PF   24-APR-2001; 2001WO-US013136.
XX
PR   25-APR-2000; 2000US-00558245.
XX
PA   (DNAS-) DNA SCI INC.
XX
PI   Xu H,  Mathies RA;
XX
DR   WPI; 2002-049286/06.
XX
PT   Analyzing variant sites in nucleic acid, useful e.g. for detecting
PT   disease-associated polymorphisms, comprises extension of labeled primer
PT   in presence of polymerase with 3'-5'-exonuclease activity.
XX
PS   Example 2; Fig 7C; 82pp; English.
XX
CC   The present sequence is that of a labelled PCR primer used to amplify and
CC   genotype the partial nucleotide sequence of lipoprotein lipase precursor
CC   (LPL) surrounding the single-nucleotide polymorphism (SNP)-5 site given
CC   in ABA02531. The specification describes a novel method for analysing a
CC   variant site (VS) in a target nucleic acid (NA). NA is amplified sequence
CC   specifically by extending two primers (P1, P2) in the presence of a
CC   polymerase having 3'-5'-exonuclease activity. P1 is labelled on at least
CC   one nucleotide (nt) other than the 3'-terminal nt and it anneals to a
CC   region that spans VS in the first strand of NA. P2 is complementary to a
CC   region in the complementary second strand of NA. If P1 is complementary
CC   to the base occupying VS it will be extended to form a labelled product.
CC   If P1 is not complementary the polymerase will digest P1 from its 3'-end,
CC   removing the label, and any extension product will be unlabelled. The
CC   extension products are analysed for absence/presence of the label. The
CC   method of the invention is particularly used to detect point mutations
CC   and SNPs, e.g. for diagnosis and prognosis of diabetes, thalassaemia,
CC   sickle-cell anaemia, cystic fibrosis or oncogenic mutations, or for
CC   assessing predisposition to these conditions or monitoring the effect of
CC   treatments. Other applications are detecting pathogens (including those
CC   with altered pathogenicity or drug resistance); resolving paternity
CC   disputes, and in prenatal testing or forensic investigations. The method
CC   can be used for simultaneous analysis of many different VS, in one or
CC   more targets, providing very high throughput and rapid genotyping
XX
SQ   Sequence 16 BP; 4 A; 6 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             59.0%;  Score 11.8;  DB 6;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6.4e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 ACTCTTGCAGGAAGC 16
              || |||||||| |||
Db          1 ACCCTTGCAGGCAGC 15


RESULT 40
AAF07158
ID   AAF07158 standard; DNA; 17 BP.
XX
AC   AAF07158;
XX
DT   16-FEB-2001  (first entry)
XX
DE   Hammerhead ribozyme substrate #3415.
XX
KW   Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW   interferon alpha; ss.
XX
OS   Homo sapiens.
XX
PN   WO200061729-A2.
XX
PD   19-OCT-2000.
XX
PF   11-APR-2000; 2000WO-US009721.
XX
PR   12-APR-1999;   99US-0129390P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Blatt L,  Zwick M,  Pavco P,  Mcswiggen J;
XX
```

DR WPI; 2000-647423/62.
XX
PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor protein,
PT interferon alpha and erythropoietin.
XX
PS Claim 54; Page 134; 164pp; English.
XX
CC The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
CC factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP).
CC Inhibition of the repressors removes prevents inhibition (and
CC consequently increases expression of) genes involved in the production of
CC erythropoietin, granulocyte colony stimulating factor protein and
CC interferon alpha
XX
SQ Sequence 17 BP; 6 A; 2 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 59.0%; Score 11.8; DB 3; Length 17;
Best Local Similarity 86.7%; Pred. No. 6.4e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAAG 15
||||.||.|||||||
Db 1 GACTATTTCAGGAAG 15

Search completed: August 6, 2005, 15:37:05
Job time : 236 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 6, 2005, 15:33:37 ; Search time 341 Seconds
(without alignments)
380.195 Million cell updates/sec

Title: US-10-773-678-342
Perfect score: 20
Sequence: 1 gactcttgcaggaagcggct 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7297361 seqs, 3241162794 residues

Total number of hits satisfying chosen parameters: 1713812

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	20	21	US-10-773-678-342	Sequence 342, App
2	19	95.0	20	21	US-10-773-678-179	Sequence 179, App
3	19	95.0	20	21	US-10-773-678-341	Sequence 341, App
4	18	90.0	20	21	US-10-773-678-343	Sequence 343, App
5	17	85.0	20	21	US-10-773-678-340	Sequence 340, App
6	17	85.0	20	21	US-10-773-678-344	Sequence 344, App
7	16	80.0	20	22	US-10-857-715-201	Sequence 201, App
8	15	75.0	20	21	US-10-773-678-339	Sequence 339, App
9	15	75.0	20	21	US-10-773-678-345	Sequence 345, App
10	14	70.0	20	9	US-09-758-881-19	Sequence 19, Appl
11	14	70.0	20	21	US-10-773-678-19	Sequence 19, Appl
c 12	13.6	68.0	20	19	US-10-671-395-1012	Sequence 1012, Ap
c 13	12.8	64.0	17	17	US-10-339-674-1350	Sequence 1350, Ap
14	12.8	64.0	18	17	US-10-339-674-1351	Sequence 1351, Ap
c 15	12.8	64.0	19	17	US-10-339-674-1348	Sequence 1348, Ap
16	12.8	64.0	19	17	US-10-339-674-1349	Sequence 1349, Ap
17	12.8	64.0	20	9	US-09-752-639-134	Sequence 134, App
18	12.8	64.0	20	9	US-09-984-198-134	Sequence 134, App
19	12.8	64.0	20	21	US-10-967-092-134	Sequence 134, App
20	12.8	64.0	20	24	US-11-011-500-134	Sequence 134, App
c 21	12.6	63.0	20	19	US-10-671-395-571	Sequence 571, App
c 22	12.6	63.0	20	19	US-10-671-395-1013	Sequence 1013, Ap
23	12.4	62.0	17	22	US-10-984-919-1512	Sequence 1512, Ap
c 24	12.4	62.0	20	14	US-10-138-316-79	Sequence 79, Appl
c 25	12.4	62.0	20	16	US-10-368-643-79	Sequence 79, Appl
c 26	12.4	62.0	20	19	US-10-714-796-129	Sequence 129, App
c 27	12.4	62.0	20	19	US-10-714-796-161	Sequence 161, App
c 28	12.4	62.0	20	20	US-10-861-520-79	Sequence 79, Appl
c 29	12.4	62.0	20	21	US-10-911-678-79	Sequence 79, Appl
30	12.2	61.0	17	9	US-09-866-108-8114	Sequence 8114, Ap
c 31	12.2	61.0	17	10	US-09-730-289B-544	Sequence 544, App
32	12.2	61.0	17	19	US-10-723-361-8114	Sequence 8114, Ap
c 33	12.2	61.0	20	19	US-10-671-395-507	Sequence 507, App
c 34	12.2	61.0	20	19	US-10-671-395-692	Sequence 692, App
c 35	12.2	61.0	20	21	US-10-719-900-383106	Sequence 383106,
c 36	12.2	61.0	20	22	US-10-719-956-271624	Sequence 271624,
c 37	12	60.0	20	17	US-10-349-143-8500	Sequence 8500, Ap
c 38	11.8	59.0	17	10	US-09-780-533A-91	Sequence 91, Appl
c 39	11.8	59.0	17	10	US-09-780-533A-92	Sequence 92, Appl
c 40	11.8	59.0	17	10	US-09-780-533A-997	Sequence 997, App
c 41	11.8	59.0	17	15	US-10-060-998-225	Sequence 225, App
c 42	11.8	59.0	17	15	US-10-060-998-226	Sequence 226, App
c 43	11.8	59.0	17	15	US-10-060-998-227	Sequence 227, App
44	11.8	59.0	19	22	US-10-888-226-346	Sequence 346, App
c 45	11.8	59.0	19	22	US-10-888-226-760	Sequence 760, App
c 46	11.8	59.0	19	22	US-10-923-522-70	Sequence 70, Appl
47	11.8	59.0	19	22	US-10-923-522-333	Sequence 333, App
c 48	11.8	59.0	20	14	US-10-181-177-130	Sequence 130, App
c 49	11.8	59.0	20	17	US-10-339-674-1183	Sequence 1183, Ap
50	11.8	59.0	20	17	US-10-339-674-1184	Sequence 1184, Ap
51	11.6	58.0	20	10	US-09-972-115A-29	Sequence 29, Appl
c 52	11.6	58.0	20	16	US-10-167-241-11	Sequence 11, Appl
c 53	11.6	58.0	20	16	US-10-168-517-8	Sequence 8, Appli
c 54	11.6	58.0	20	16	US-10-369-378-38	Sequence 38, Appl
55	11.6	58.0	20	16	US-10-369-378-39	Sequence 39, Appl
c 56	11.6	58.0	20	16	US-10-199-937-173	Sequence 173, App
57	11.6	58.0	20	16	US-10-199-937-174	Sequence 174, App
c 58	11.6	58.0	20	17	US-10-181-874-49	Sequence 49, Appl
c 59	11.6	58.0	20	17	US-10-380-873B-18	Sequence 18, Appl
c 60	11.6	58.0	20	18	US-10-168-853-8	Sequence 8, Appli
c 61	11.6	58.0	20	19	US-10-671-395-340	Sequence 340, App
c 62	11.4	57.0	15	19	US-10-698-689-110	Sequence 110, App
c 63	11.4	57.0	15	21	US-10-946-498A-12	Sequence 12, Appl
64	11.4	57.0	15	22	US-10-984-919-1599	Sequence 1599, Ap
c 65	11.4	57.0	15	22	US-10-763-367A-13	Sequence 13, Appl
c 66	11.4	57.0	16	17	US-10-415-247-8	Sequence 8, Appli
67	11.4	57.0	17	9	US-09-866-108-115	Sequence 115, App
68	11.4	57.0	17	9	US-09-866-108-116	Sequence 116, App
69	11.4	57.0	17	9	US-09-866-108-117	Sequence 117, App
70	11.4	57.0	17	9	US-09-866-108-118	Sequence 118, App
71	11.4	57.0	17	9	US-09-866-108-119	Sequence 119, App
c 72	11.4	57.0	17	9	US-09-866-108-6215	Sequence 6215, Ap
c 73	11.4	57.0	17	9	US-09-866-108-6216	Sequence 6216, Ap
c 74	11.4	57.0	17	9	US-09-866-108-6217	Sequence 6217, Ap
c 75	11.4	57.0	17	9	US-09-866-108-6218	Sequence 6218, Ap
c 76	11.4	57.0	17	9	US-09-866-108-6219	Sequence 6219, Ap
c 77	11.4	57.0	17	14	US-10-060-830-121	Sequence 121, App
c 78	11.4	57.0	17	14	US-10-060-830-122	Sequence 122, App
c 79	11.4	57.0	17	14	US-10-060-830-123	Sequence 123, App
c 80	11.4	57.0	17	14	US-10-060-830-124	Sequence 124, App

c	81	11.4	57.0	17	14	US-10-060-830-125	Sequence 125, App
	82	11.4	57.0	17	19	US-10-723-361-115	Sequence 115, App
	83	11.4	57.0	17	19	US-10-723-361-116	Sequence 116, App
	84	11.4	57.0	17	19	US-10-723-361-117	Sequence 117, App
	85	11.4	57.0	17	19	US-10-723-361-118	Sequence 118, App
	86	11.4	57.0	17	19	US-10-723-361-119	Sequence 119, App
c	87	11.4	57.0	17	19	US-10-723-361-6215	Sequence 6215, Ap
c	88	11.4	57.0	17	19	US-10-723-361-6216	Sequence 6216, Ap
c	89	11.4	57.0	17	19	US-10-723-361-6217	Sequence 6217, Ap
c	90	11.4	57.0	17	19	US-10-723-361-6218	Sequence 6218, Ap
c	91	11.4	57.0	17	19	US-10-723-361-6219	Sequence 6219, Ap
	92	11.4	57.0	20	10	US-09-906-158-19	Sequence 19, Appl
	93	11.4	57.0	20	17	US-10-388-263-468	Sequence 468, App
	94	11.4	57.0	20	17	US-10-289-762-6247	Sequence 6247, Ap
	95	11.4	57.0	20	17	US-10-363-198-51	Sequence 51, Appl
	96	11.4	57.0	20	19	US-10-316-516-76	Sequence 76, Appl
c	97	11.4	57.0	20	19	US-10-316-516-129	Sequence 129, App
	98	11.4	57.0	20	19	US-10-714-796-168	Sequence 168, App
c	99	11.4	57.0	20	22	US-10-257-158A-7002	Sequence 7002, Ap
	100	11.4	57.0	20	24	US-11-039-629-253	Sequence 253, App

ALIGNMENTS

RESULT 1
US-10-773-678-342
; Sequence 342, Application US/10773678
; Publication No. US20050074879A1
; GENERAL INFORMATION:
; APPLICANT: Karras, James G
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
; TITLE OF INVENTION: Expression
; FILE REFERENCE: ISPH-0828
; CURRENT APPLICATION NUMBER: US/10/773,678
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 10/713,139
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 09/758,881
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/09054
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/288,461
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 402
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 342
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-10-773-678-342

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GACTCTTGCAGGAAGCGGCT 20
              ||||||||||||||||||||
Db          1 GACTCTTGCAGGAAGCGGCT 20
```

RESULT 2
US-10-773-678-179
; Sequence 179, Application US/10773678
; Publication No. US20050074879A1
; GENERAL INFORMATION:
; APPLICANT: Karras, James G
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
; TITLE OF INVENTION: Expression
; FILE REFERENCE: ISPH-0828
; CURRENT APPLICATION NUMBER: US/10/773,678
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 10/713,139
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 09/758,881
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/09054
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/288,461
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 402
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 179
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-10-773-678-179

Query Match 95.0%; Score 19; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GACTCTTGCAGGAAGCGGC 19
              |||||||||||||||||||
Db          2 GACTCTTGCAGGAAGCGGC 20
```

RESULT 3
US-10-773-678-341
; Sequence 341, Application US/10773678
; Publication No. US20050074879A1
; GENERAL INFORMATION:
; APPLICANT: Karras, James G
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
; TITLE OF INVENTION: Expression
; FILE REFERENCE: ISPH-0828
; CURRENT APPLICATION NUMBER: US/10/773,678
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 10/713,139
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 09/758,881
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/09054
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/288,461
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 402
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 341
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-10-773-678-341

Query Match 95.0%; Score 19; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 ACTCTTGCAGGAAGCGGCT 20
              |||||||||||||||||||
Db          1 ACTCTTGCAGGAAGCGGCT 19
```

RESULT 4
US-10-773-678-343
; Sequence 343, Application US/10773678
; Publication No. US20050074879A1
; GENERAL INFORMATION:
; APPLICANT: Karras, James G
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3

```
;  TITLE OF INVENTION:  Expression
;  FILE REFERENCE: ISPH-0828
;  CURRENT APPLICATION NUMBER: US/10/773,678
;  CURRENT FILING DATE:  2004-02-06
;  PRIOR APPLICATION NUMBER: 10/713,139
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 09/758,881
;  PRIOR FILING DATE: 2001-01-11
;  PRIOR APPLICATION NUMBER: PCT/US00/09054
;  PRIOR FILING DATE: 2000-04-06
;  PRIOR APPLICATION NUMBER: 09/288,461
;  PRIOR FILING DATE: 1999-04-08
;  NUMBER OF SEQ ID NOS: 402
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 343
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense oligonucleotide
US-10-773-678-343

  Query Match             90.0%;  Score 18;  DB 21;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GACTCTTGCAGGAAGCGG 18
              ||||||||||||||||||
Db          3 GACTCTTGCAGGAAGCGG 20


RESULT 5
US-10-773-678-340
; Sequence 340, Application US/10773678
; Publication No. US20050074879A1
; GENERAL INFORMATION:
;  APPLICANT: Karras, James G
;  TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
;  TITLE OF INVENTION:  Expression
;  FILE REFERENCE: ISPH-0828
;  CURRENT APPLICATION NUMBER: US/10/773,678
;  CURRENT FILING DATE:  2004-02-06
;  PRIOR APPLICATION NUMBER: 10/713,139
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 09/758,881
;  PRIOR FILING DATE: 2001-01-11
;  PRIOR APPLICATION NUMBER: PCT/US00/09054
;  PRIOR FILING DATE: 2000-04-06
;  PRIOR APPLICATION NUMBER: 09/288,461
;  PRIOR FILING DATE: 1999-04-08
;  NUMBER OF SEQ ID NOS: 402
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 340
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense oligonucleotide
US-10-773-678-340

  Query Match             85.0%;  Score 17;  DB 21;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 TCTTGCAGGAAGCGGCT 20
              |||||||||||||||||
Db          1 TCTTGCAGGAAGCGGCT 17


RESULT 6
US-10-773-678-344
; Sequence 344, Application US/10773678
; Publication No. US20050074879A1
; GENERAL INFORMATION:
;  APPLICANT: Karras, James G
;  TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
;  TITLE OF INVENTION:  Expression
;  FILE REFERENCE: ISPH-0828
;  CURRENT APPLICATION NUMBER: US/10/773,678
;  CURRENT FILING DATE:  2004-02-06
;  PRIOR APPLICATION NUMBER: 10/713,139
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 09/758,881
;  PRIOR FILING DATE: 2001-01-11
;  PRIOR APPLICATION NUMBER: PCT/US00/09054
;  PRIOR FILING DATE: 2000-04-06
;  PRIOR APPLICATION NUMBER: 09/288,461
;  PRIOR FILING DATE: 1999-04-08
;  NUMBER OF SEQ ID NOS: 402
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 344
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense oligonucleotide
US-10-773-678-344

  Query Match             85.0%;  Score 17;  DB 21;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GACTCTTGCAGGAAGCG 17
              |||||||||||||||||
Db          4 GACTCTTGCAGGAAGCG 20


RESULT 7
US-10-857-715-201
; Sequence 201, Application US/10857715
; Publication No. US20050164218A1
; GENERAL INFORMATION:
;  APPLICANT: Agus David
;  APPLICANT:  Baker Joffre
;  APPLICANT:  Natale Ron
;  APPLICANT:  Shak Steven
;  TITLE OF INVENTION: Gene Expression Markers for Response to
;  TITLE OF INVENTION:  EGFR Inhibitors Drugs
;  FILE REFERENCE: 39740/0011
;  CURRENT APPLICATION NUMBER: US/10/857,715
;  CURRENT FILING DATE:  2004-05-28
;  PRIOR APPLICATION NUMBER: 60/474,908
;  PRIOR FILING DATE: 2003-05-30
;  NUMBER OF SEQ ID NOS: 232
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 201
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: reverse primer
US-10-857-715-201

  Query Match             80.0%;  Score 16;  DB 22;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CTTGCAGGAAGCGGCT 20
              ||||||||||||||||
Db          1 CTTGCAGGAAGCGGCT 16


RESULT 8
US-10-773-678-339
; Sequence 339, Application US/10773678
; Publication No. US20050074879A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: Karras, James G
;  TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
;  TITLE OF INVENTION:  Expression
;  FILE REFERENCE: ISPH-0828
;  CURRENT APPLICATION NUMBER: US/10/773,678
;  CURRENT FILING DATE:  2004-02-06
;  PRIOR APPLICATION NUMBER: 10/713,139
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 09/758,881
;  PRIOR FILING DATE: 2001-01-11
;  PRIOR APPLICATION NUMBER: PCT/US00/09054
;  PRIOR FILING DATE: 2000-04-06
;  PRIOR APPLICATION NUMBER: 09/288,461
;  PRIOR FILING DATE: 1999-04-08
;  NUMBER OF SEQ ID NOS: 402
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 339
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense oligonucleotide
US-10-773-678-339

  Query Match             75.0%;  Score 15;  DB 21;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 TTGCAGGAAGCGGCT 20
              |||||||||||||||
Db          1 TTGCAGGAAGCGGCT 15


RESULT 9
US-10-773-678-345
; Sequence 345, Application US/10773678
; Publication No. US20050074879A1
; GENERAL INFORMATION:
;  APPLICANT: Karras, James G
;  TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
;  TITLE OF INVENTION:  Expression
;  FILE REFERENCE: ISPH-0828
;  CURRENT APPLICATION NUMBER: US/10/773,678
;  CURRENT FILING DATE:  2004-02-06
;  PRIOR APPLICATION NUMBER: 10/713,139
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 09/758,881
;  PRIOR FILING DATE: 2001-01-11
;  PRIOR APPLICATION NUMBER: PCT/US00/09054
;  PRIOR FILING DATE: 2000-04-06
;  PRIOR APPLICATION NUMBER: 09/288,461
;  PRIOR FILING DATE: 1999-04-08
;  NUMBER OF SEQ ID NOS: 402
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 345
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense oligonucleotide
US-10-773-678-345

  Query Match             75.0%;  Score 15;  DB 21;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GACTCTTGCAGGAAG 15
              |||||||||||||||
Db          6 GACTCTTGCAGGAAG 20


RESULT 10
US-09-758-881-19
; Sequence 19, Application US/09758881
; Patent No. US20010029250A1
; GENERAL INFORMATION:
;  APPLICANT:  Karras, James G
;  TITLE OF INVENTION:  Antisense Oligonucleotide Modulation of STAT3
;  TITLE OF INVENTION:  Expression
;  FILE REFERENCE:  ISPH-0532
;  CURRENT APPLICATION NUMBER: US/09/758,881
;  CURRENT FILING DATE:  2001-01-11
;  PRIOR APPLICATION NUMBER:  PCT/US00/09054
;  PRIOR FILING DATE:  2000-04-06
;  PRIOR APPLICATION NUMBER:  09/288,461
;  PRIOR FILING DATE:  1999-04-08
;  NUMBER OF SEQ ID NOS:  152
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 19
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-758-881-19

  Query Match             70.0%;  Score 14;  DB 9;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GACTCTTGCAGGAA 14
              ||||||||||||||
Db          7 GACTCTTGCAGGAA 20


RESULT 11
US-10-773-678-19
; Sequence 19, Application US/10773678
; Publication No. US20050074879A1
; GENERAL INFORMATION:
;  APPLICANT: Karras, James G
;  TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
;  TITLE OF INVENTION:  Expression
;  FILE REFERENCE: ISPH-0828
;  CURRENT APPLICATION NUMBER: US/10/773,678
;  CURRENT FILING DATE:  2004-02-06
;  PRIOR APPLICATION NUMBER: 10/713,139
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 09/758,881
;  PRIOR FILING DATE: 2001-01-11
;  PRIOR APPLICATION NUMBER: PCT/US00/09054
;  PRIOR FILING DATE: 2000-04-06
;  PRIOR APPLICATION NUMBER: 09/288,461
;  PRIOR FILING DATE: 1999-04-08
;  NUMBER OF SEQ ID NOS: 402
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-773-678-19

  Query Match             70.0%;  Score 14;  DB 21;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GACTCTTGCAGGAA 14
              ||||||||||||||
Db          7 GACTCTTGCAGGAA 20


RESULT 12
US-10-671-395-1012/c
```

```
; Sequence 1012, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Gierse, James K
;  TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: 1179/1/US
;  CURRENT APPLICATION NUMBER: US/10/671,395
;  CURRENT FILING DATE:  2003-09-25
;  PRIOR APPLICATION NUMBER: 60/413,549
;  PRIOR FILING DATE: 2002-09-25
;  NUMBER OF SEQ ID NOS: 1809
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1012
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1012

  Query Match             68.0%;  Score 13.6;  DB 19;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 4.4e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GACTCTTGCAGGAAGCGGCT 20
              || || |||| |||| ||||
Db         20 GATTCCTGCACGAAGTGGCT 1


RESULT 13
US-10-339-674-1350/c
; Sequence 1350, Application US/10339674
; Publication No. US20030204318A1
; GENERAL INFORMATION:
;  APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
;  TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
;  FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
;  CURRENT APPLICATION NUMBER: US/10/339,674
;  CURRENT FILING DATE:  2003-06-06
;  NUMBER OF SEQ ID NOS: 3537
;  SOFTWARE: Proprietary
; SEQ ID NO 1350
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Escherichia coli K-12 MG1655 complete genome.
;   FEATURE:
;   LOCATION: (1734068)...(1734084)
;   OTHER INFORMATION: Chromosome = 1  Strand = positive  ConnectronObjectNumber =  1777
US-10-339-674-1350

  Query Match             64.0%;  Score 12.8;  DB 17;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 1.1e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 TCTTGCAGGAAGCGGC 19
              |||||| ||| |||||
Db         17 TCTTGCCGGATGCGGC 2


RESULT 14
US-10-339-674-1351
; Sequence 1351, Application US/10339674
; Publication No. US20030204318A1
; GENERAL INFORMATION:
;  APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
;  TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
;  FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
;  CURRENT APPLICATION NUMBER: US/10/339,674
;  CURRENT FILING DATE:  2003-06-06
;  NUMBER OF SEQ ID NOS: 3537
;  SOFTWARE: Proprietary
; SEQ ID NO 1351
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Escherichia coli K-12 MG1655 complete genome.
;   FEATURE:
;   LOCATION: (1734068)...(1734085)
;   OTHER INFORMATION: Chromosome = 1  Strand = negative  ConnectronObjectNumber =  1778
US-10-339-674-1351

  Query Match             64.0%;  Score 12.8;  DB 17;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 1.1e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 TCTTGCAGGAAGCGGC 19
              |||||| ||| |||||
Db          2 TCTTGCCGGATGCGGC 17


RESULT 15
US-10-339-674-1348/c
; Sequence 1348, Application US/10339674
; Publication No. US20030204318A1
; GENERAL INFORMATION:
;  APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
;  TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
;  FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
;  CURRENT APPLICATION NUMBER: US/10/339,674
;  CURRENT FILING DATE:  2003-06-06
;  NUMBER OF SEQ ID NOS: 3537
;  SOFTWARE: Proprietary
; SEQ ID NO 1348
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Escherichia coli K-12 MG1655 complete genome.
;   FEATURE:
;   LOCATION: (1734067)...(1734085)
;   OTHER INFORMATION: Chromosome = 1  Strand = positive  ConnectronObjectNumber =  177
US-10-339-674-1348

  Query Match             64.0%;  Score 12.8;  DB 17;  Length 19;
  Best Local Similarity   87.5%;  Pred. No. 1.1e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 TCTTGCAGGAAGCGGC 19
              |||||| ||| |||||
Db         18 TCTTGCCGGATGCGGC 3


RESULT 16
US-10-339-674-1349
; Sequence 1349, Application US/10339674
; Publication No. US20030204318A1
; GENERAL INFORMATION:
;  APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
;  TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
;  FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
;  CURRENT APPLICATION NUMBER: US/10/339,674
;  CURRENT FILING DATE:  2003-06-06
;  NUMBER OF SEQ ID NOS: 3537
;  SOFTWARE: Proprietary
; SEQ ID NO 1349
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Escherichia coli K-12 MG1655 complete genome.
;   FEATURE:
;   LOCATION: (1734067)...(1734085)
;   OTHER INFORMATION: Chromosome = 1  Strand = negative  ConnectronObjectNumber =  177
US-10-339-674-1349

  Query Match             64.0%;  Score 12.8;  DB 17;  Length 19;
  Best Local Similarity   87.5%;  Pred. No. 1.1e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
```

```
Qy          4 TCTTGCAGGAAGCGGC 19
              |||||| ||| |||||
Db          2 TCTTGCCGGATGCGGC 17


RESULT 17
US-09-752-639-134
; Sequence 134, Application US/09752639
; Patent No. US20020091243A1
;  GENERAL INFORMATION:
;    APPLICANT:  Gatanaga, T.
;    APPLICANT:  Granger, G.A.
;    TITLE OF INVENTION:  Factors Altering Tumor Necrosis
;    TITLE OF INVENTION:  Factor Receptor Releasing Enzyme Activity, and Methods
;    TITLE OF INVENTION:  of Use Thereof
;    NUMBER OF SEQUENCES:  154
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 PAGE MILL ROAD
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/752,639
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US99/10793
;      FILING DATE:
;      APPLICATION NUMBER:  09/081,385
;      FILING DATE:
;      APPLICATION NUMBER:  08/964,747
;      FILING DATE:  05-NOV-1997
;      APPLICATION NUMBER:  60/030,761
;      FILING DATE:  06-NOV-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wu, Frank
;      REGISTRATION NUMBER:  41,386
;      REFERENCE/DOCKET NUMBER:  22000-20577.21
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-813-5600
;      TELEFAX:  650-494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  134:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-752-639-134

  Query Match             64.0%;  Score 12.8;  DB 9;  Length 20;
  Best Local Similarity   87.5%;  Pred. No. 1.1e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 TCTTGCAGGAAGCGGC 19
              |||| |||||||| ||
Db          1 TCTTCCAGGAAGCTGC 16


RESULT 18
US-09-984-198-134
; Sequence 134, Application US/09984198
; Patent No. US20020106679A1
;  GENERAL INFORMATION:
;    APPLICANT:  Gatanaga, T.
;    APPLICANT:  Granger, G.A.
;    TITLE OF INVENTION:  Factors Altering Tumor Necrosis
;    TITLE OF INVENTION:  Factor Receptor Releasing Enzyme Activity, and Methods
;    TITLE OF INVENTION:  of Use Thereof
;    NUMBER OF SEQUENCES:  154
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 PAGE MILL ROAD
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/984,198
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US99/10793
;      FILING DATE:
;      APPLICATION NUMBER:  09/081,385
;      FILING DATE:
;      APPLICATION NUMBER:  08/964,747
;      FILING DATE:  05-NOV-1997
;      APPLICATION NUMBER:  60/030,761
;      FILING DATE:  06-NOV-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wu, Frank
;      REGISTRATION NUMBER:  41,386
;      REFERENCE/DOCKET NUMBER:  22000-20577.21
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-813-5600
;      TELEFAX:  650-494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  134:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-984-198-134

  Query Match             64.0%;  Score 12.8;  DB 9;  Length 20;
  Best Local Similarity   87.5%;  Pred. No. 1.1e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 TCTTGCAGGAAGCGGC 19
              |||| |||||||| ||
Db          1 TCTTCCAGGAAGCTGC 16


RESULT 19
US-10-967-092-134
; Sequence 134, Application US/10967092
; Publication No. US20050090647A1
;  GENERAL INFORMATION:
;       APPLICANT: Gatanaga, T.
;                  Granger, G.A.
;       TITLE OF INVENTION: Factors Altering Tumor Necrosis
;                           Factor Receptor Releasing Enzyme Activity, and Methods
;                           of Use Thereof
;       NUMBER OF SEQUENCES: 154
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: MORRISON & FOERSTER
;            STREET: 755 PAGE MILL ROAD
;            CITY: Palo Alto
;            STATE: CA
;            COUNTRY: USA
;            ZIP: 94304-1018
;       COMPUTER READABLE FORM:
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;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: Windows
;             SOFTWARE: FastSEQ for Windows Version 2.0b
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/967,092
;             FILING DATE: 15-Oct-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/712,813
;             FILING DATE: 13-Nov-2000
;             APPLICATION NUMBER: US/09/081,385
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: 08/964,747
;             FILING DATE: 05-NOV-1997
;             APPLICATION NUMBER: 60/030,761
;             FILING DATE: 06-NOV-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Wu, Frank
;             REGISTRATION NUMBER: 41,386
;             REFERENCE/DOCKET NUMBER: 22000-20577.21
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650-813-5600
;             TELEFAX: 650-494-0792
;             TELEX: 706141
;   INFORMATION FOR SEQ ID NO: 134:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 20 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 134:
US-10-967-092-134

  Query Match             64.0%;  Score 12.8;  DB 21;  Length 20;
  Best Local Similarity   87.5%;  Pred. No. 1.1e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 TCTTGCAGGAAGCGGC 19
              |||| |||||||| ||
Db          1 TCTTCCAGGAAGCTGC 16


RESULT 20
US-11-011-500-134
; Sequence 134, Application US/11011500
; Publication No. US20050158826A1
;  GENERAL INFORMATION:
;       APPLICANT: Gatanaga, T.
;                  Granger, G.A.
;       TITLE OF INVENTION: Factors Altering Tumor Necrosis
;                           Factor Receptor Releasing Enzyme Activity, and Methods
;                           of Use Thereof
;       NUMBER OF SEQUENCES: 154
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: MORRISON & FOERSTER
;            STREET: 755 PAGE MILL ROAD
;            CITY: Palo Alto
;            STATE: CA
;            COUNTRY: USA
;            ZIP: 94304-1018
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: Windows
;            SOFTWARE: FastSEQ for Windows Version 2.0b
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/11/011,500
;            FILING DATE: 13-Dec-2004
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/10/967,092
;            FILING DATE: 15-Oct-2004
;            APPLICATION NUMBER: US/09/712,813
;            FILING DATE: 13-Nov-2000
;            APPLICATION NUMBER: US/09/081,385
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: 08/964,747
;            FILING DATE: 05-NOV-1997
;            APPLICATION NUMBER: 60/030,761
;            FILING DATE: 06-NOV-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Wu, Frank
;            REGISTRATION NUMBER: 41,386
;            REFERENCE/DOCKET NUMBER: 22000-20577.21
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 650-813-5600
;            TELEFAX: 650-494-0792
;            TELEX: 706141
;   INFORMATION FOR SEQ ID NO: 134:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 20 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 134:
US-11-011-500-134

  Query Match             64.0%;  Score 12.8;  DB 24;  Length 20;
  Best Local Similarity   87.5%;  Pred. No. 1.1e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 TCTTGCAGGAAGCGGC 19
              |||| |||||||| ||
Db          1 TCTTCCAGGAAGCTGC 16


RESULT 21
US-10-671-395-571/c
; Sequence 571, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Gierse, James K
;  TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: 1179/1/US
;  CURRENT APPLICATION NUMBER: US/10/671,395
;  CURRENT FILING DATE:  2003-09-25
;  PRIOR APPLICATION NUMBER: 60/413,549
;  PRIOR FILING DATE: 2002-09-25
;  NUMBER OF SEQ ID NOS: 1809
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 571
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-571

  Query Match             63.0%;  Score 12.6;  DB 19;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 1.5e+04;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GACTCTTGCAGGAAGCGGC 19
              || || |||| |||| |||
Db         19 GATTCCTGCACGAAGTGGC 1


RESULT 22
US-10-671-395-1013/c
; Sequence 1013, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
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```
;  APPLICANT:  Gierse, James K
;  TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: 1179/1/US
;  CURRENT APPLICATION NUMBER: US/10/671,395
;  CURRENT FILING DATE:  2003-09-25
;  PRIOR APPLICATION NUMBER: 60/413,549
;  PRIOR FILING DATE: 2002-09-25
;  NUMBER OF SEQ ID NOS: 1809
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1013
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1013

  Query Match            63.0%;  Score 12.6;  DB 19;  Length 20;
  Best Local Similarity  78.9%;  Pred. No. 1.5e+04;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 ACTCTTGCAGGAAGCGGCT 20
              | || |||| |||| ||||
Db         20 ATTCCTGCACGAAGTGGCT 2


RESULT 23
US-10-984-919-1512
; Sequence 1512, Application US/10984919
; Publication No. US20050130927A1
; GENERAL INFORMATION:
;  APPLICANT: Schlingensiepen, Karl-Hermann
;  APPLICANT:  Brysch, Wolfgang
;  TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
;  FILE REFERENCE: 10496/P63763USO
;  CURRENT APPLICATION NUMBER: US/10/984,919
;  CURRENT FILING DATE:  2004-11-10
;  PRIOR APPLICATION NUMBER: US/09/341,700
;  PRIOR FILING DATE: 1999-09-24
;  PRIOR APPLICATION NUMBER: PCT/EP98/00497
;  PRIOR FILING DATE: 1998-01-30
;  PRIOR APPLICATION NUMBER: EP 97 101 531.8
;  PRIOR FILING DATE: 1997-01-31
;  NUMBER OF SEQ ID NOS: 1764
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1512
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: antisense oligonucleotide
US-10-984-919-1512

  Query Match            62.0%;  Score 12.4;  DB 22;  Length 17;
  Best Local Similarity  92.9%;  Pred. No. 1.9e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 ACTCTTGCAGGAAG 15
              |||||||||| ||
Db          4 ACTCTTGCAGGTAG 17


RESULT 24
US-10-138-316-79/c
; Sequence 79, Application US/10138316
; Publication No. US20030054380A1
; GENERAL INFORMATION:
;  APPLICANT: Keating, Mark T.
;  APPLICANT:  Sanguinetti, Michael C.
;  APPLICANT:  Splawski, Igor
;  TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN minK WHICH
;  TITLE OF INVENTION:  CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
;  TITLE OF INVENTION:  KCNE1 AS AN LQT GENE
;  FILE REFERENCE: 2323-162
;  CURRENT APPLICATION NUMBER: US/10/138,316
;  CURRENT FILING DATE:  2002-05-06
;  PRIOR APPLICATION NUMBER: 09/444,295
;  PRIOR FILING DATE: 1999-11-22
;  PRIOR APPLICATION NUMBER: 09/135,020
;  PRIOR FILING DATE: 1998-08-17
;  PRIOR APPLICATION NUMBER: 08/921,068
;  PRIOR FILING DATE: 1997-08-29
;  PRIOR APPLICATION NUMBER: 08/739,383
;  PRIOR FILING DATE: 1996-10-29
;  PRIOR APPLICATION NUMBER: 60/019,014
;  PRIOR FILING DATE: 1995-12-22
;  PRIOR APPLICATION NUMBER: 60/094,477
;  PRIOR FILING DATE: 1998-07-29
;  NUMBER OF SEQ ID NOS: 114
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 79
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-138-316-79

  Query Match            62.0%;  Score 12.4;  DB 14;  Length 20;
  Best Local Similarity  92.9%;  Pred. No. 1.9e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 TGCAGGAAGCGGCT 20
              |||||||||||| |
Db         18 TGCAGGAAGCGGAT 5


RESULT 25
US-10-368-643-79/c
; Sequence 79, Application US/10368643
; Publication No. US20030170708A1
; GENERAL INFORMATION:
;  APPLICANT: Keating, Mark T.
;  APPLICANT:  Sanguinetti, Michael C.
;  APPLICANT:  Curran, Mark E.
;  APPLICANT:  Landes, Gregory M.
;  APPLICANT:  Connors, Timothy D.
;  APPLICANT:  Burn, Timothy C.
;  APPLICANT:  Splawski, Igor
;  TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE
;  FILE REFERENCE: 2323-163
;  CURRENT APPLICATION NUMBER: US/10/368,643
;  CURRENT FILING DATE:  2003-02-20
;  PRIOR APPLICATION NUMBER: US 09/597,731
;  PRIOR FILING DATE: 2000-06-19
;  PRIOR APPLICATION NUMBER: US 09/135,010
;  PRIOR FILING DATE: 1998-08-17
;  PRIOR APPLICATION NUMBER: US 60/094,477
;  PRIOR FILING DATE: 1998-07-29
;  PRIOR APPLICATION NUMBER: US 08/921,068
;  PRIOR FILING DATE: 1997-08-29
;  PRIOR APPLICATION NUMBER: US 08/739,383
;  PRIOR FILING DATE: 1996-10-29
;  PRIOR APPLICATION NUMBER: US 60/019,014
;  PRIOR FILING DATE: 1995-12-22
;  NUMBER OF SEQ ID NOS: 116
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 79
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-368-643-79

  Query Match            62.0%;  Score 12.4;  DB 16;  Length 20;
  Best Local Similarity  92.9%;  Pred. No. 1.9e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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```
Qy          7 TGCAGGAAGCGGCT 20
              ||||||||||||| |
Db         18 TGCAGGAAGCGGAT 5


RESULT 26
US-10-714-796-129/c
; Sequence 129, Application US/10714796
; Publication No. US20040180847A1
; GENERAL INFORMATION:
;  APPLICANT: Dobie, Kenneth W.
;  APPLICANT:  Koller, Erich
;  TITLE OF INVENTION: ANTISENSE MODULATION OF KINESIN-LIKE 1 EXPRESSION
;  FILE REFERENCE: ISHT-1004
;  CURRENT APPLICATION NUMBER: US/10/714,796
;  CURRENT FILING DATE:  2003-11-17
;  PRIOR APPLICATION NUMBER: US 10/156,603
;  PRIOR FILING DATE: 2002-05-23
;  NUMBER OF SEQ ID NOS: 237
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 129
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-714-796-129

  Query Match             62.0%;  Score 12.4;  DB 19;  Length 20;
  Best Local Similarity   92.9%;  Pred. No. 1.9e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TCTTGCAGGAAGCG 17
              ||||||||||||| |
Db         20 TCTTGCAGGAAGTG 7


RESULT 27
US-10-714-796-161/c
; Sequence 161, Application US/10714796
; Publication No. US20040180847A1
; GENERAL INFORMATION:
;  APPLICANT: Dobie, Kenneth W.
;  APPLICANT:  Koller, Erich
;  TITLE OF INVENTION: ANTISENSE MODULATION OF KINESIN-LIKE 1 EXPRESSION
;  FILE REFERENCE: ISHT-1004
;  CURRENT APPLICATION NUMBER: US/10/714,796
;  CURRENT FILING DATE:  2003-11-17
;  PRIOR APPLICATION NUMBER: US 10/156,603
;  PRIOR FILING DATE: 2002-05-23
;  NUMBER OF SEQ ID NOS: 237
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 161
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-714-796-161

  Query Match             62.0%;  Score 12.4;  DB 19;  Length 20;
  Best Local Similarity   92.9%;  Pred. No. 1.9e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TCTTGCAGGAAGCG 17
              ||||||||||||| |
Db         19 TCTTGCAGGAAGTG 6


RESULT 28
US-10-861-520-79/c
; Sequence 79, Application US/10861520
; Publication No. US20040235038A1
; GENERAL INFORMATION:
;  APPLICANT: Keating, Mark T.
;  APPLICANT:  Sanguinetti, Michael C.
;  APPLICANT:  Splawski, Igor
;  TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN minK WHICH
;  TITLE OF INVENTION:  CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
;  TITLE OF INVENTION:  KCNE1 AS AN LQT GENE
;  FILE REFERENCE: 2323-167
;  CURRENT APPLICATION NUMBER: US/10/861,520
;  CURRENT FILING DATE:  2004-06-07
;  PRIOR APPLICATION NUMBER: 10/138,316
;  PRIOR FILING DATE: 2002-05-06
;  PRIOR APPLICATION NUMBER: 09/444,295
;  PRIOR FILING DATE: 1999-11-22
;  PRIOR APPLICATION NUMBER: 09/135,020
;  PRIOR FILING DATE: 1998-08-17
;  PRIOR APPLICATION NUMBER: 08/921,068
;  PRIOR FILING DATE: 1997-08-29
;  PRIOR APPLICATION NUMBER: 08/739,383
;  PRIOR FILING DATE: 1996-10-29
;  PRIOR APPLICATION NUMBER: 60/019,014
;  PRIOR FILING DATE: 1995-12-22
;  PRIOR APPLICATION NUMBER: 60/094,477
;  PRIOR FILING DATE: 1998-07-29
;  NUMBER OF SEQ ID NOS: 114
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 79
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-861-520-79

  Query Match             62.0%;  Score 12.4;  DB 20;  Length 20;
  Best Local Similarity   92.9%;  Pred. No. 1.9e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 TGCAGGAAGCGGCT 20
              ||||||||||||| |
Db         18 TGCAGGAAGCGGAT 5


RESULT 29
US-10-911-678-79/c
; Sequence 79, Application US/10911678
; Publication No. US20050003439A1
; GENERAL INFORMATION:
;  APPLICANT: Keating, Mark T.
;  APPLICANT:  Sanguinetti, Michael C.
;  APPLICANT:  Splawski, Igor
;  TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN minK WHICH
;  TITLE OF INVENTION:  CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
;  TITLE OF INVENTION:  KCNE1 AS AN LQT GENE
;  FILE REFERENCE: 2323-169
;  CURRENT APPLICATION NUMBER: US/10/911,678
;  CURRENT FILING DATE:  2004-08-05
;  PRIOR APPLICATION NUMBER: 10/138,316
;  PRIOR FILING DATE: 2002-05-06
;  PRIOR APPLICATION NUMBER: 09/444,295
;  PRIOR FILING DATE: 1999-11-22
;  PRIOR APPLICATION NUMBER: 09/135,020
;  PRIOR FILING DATE: 1998-08-17
;  PRIOR APPLICATION NUMBER: 08/921,068
;  PRIOR FILING DATE: 1997-08-29
;  PRIOR APPLICATION NUMBER: 08/739,383
;  PRIOR FILING DATE: 1996-10-29
;  PRIOR APPLICATION NUMBER: 60/019,014
;  PRIOR FILING DATE: 1995-12-22
;  PRIOR APPLICATION NUMBER: 60/094,477
;  PRIOR FILING DATE: 1998-07-29
;  NUMBER OF SEQ ID NOS: 114
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 79
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-911-678-79
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  Query Match             62.0%;  Score 12.4;  DB 21;  Length 20;
  Best Local Similarity   92.9%;  Pred. No. 1.9e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 TGCAGGAAGCGGCT 20
              ||||||||||||| |
Db         18 TGCAGGAAGCGGAT 5


RESULT 30
US-09-866-108-8114
; Sequence 8114, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 8114
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-8114

  Query Match             61.0%;  Score 12.2;  DB 9;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 2.4e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 TCTTGCAGGAAGCGGCT 20
              || |||  |||||||||
Db          1 TCCTGCCAGAAGCGGCT 17


RESULT 31
US-09-730-289B-544/c
; Sequence 544, Application US/09730289B
; Publication No. US20030050259A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Blatt, Larry
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease
;  FILE REFERENCE: MBHB00-864-A (400/006)
;  CURRENT APPLICATION NUMBER: US/09/730,289B
;  CURRENT FILING DATE:  2000-12-05
;  PRIOR APPLICATION NUMBER: US 60/169,100
;  PRIOR FILING DATE: 1999-12-06
;  NUMBER OF SEQ ID NOS: 3897
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 544
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-730-289B-544

  Query Match             61.0%;  Score 12.2;  DB 10;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 2.4e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 ACTCTTGCAGGAAGCGG 18
              |||||| |||||| ||
Db         17 ACTCTTCTAGGAAGTGG 1


RESULT 32
US-10-723-361-8114
; Sequence 8114, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
;  FILE REFERENCE: PB0105
;  CURRENT APPLICATION NUMBER: US/10/723,361
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: US 09/866,108
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 15755
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 8114
;   LENGTH: 17
;   TYPE: DNA
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;   ORGANISM: Homo sapiens
US-10-723-361-8114

  Query Match             61.0%;  Score 12.2;  DB 19;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 2.4e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 TCTTGCAGGAAGCGGCT 20
              || |||  |||||||||
Db          1 TCCTGCCAGAAGCGGCT 17


RESULT 33
US-10-671-395-507/c
; Sequence 507, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Gierse, James K
;  TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: 1179/1/US
;  CURRENT APPLICATION NUMBER: US/10/671,395
;  CURRENT FILING DATE:  2003-09-25
;  PRIOR APPLICATION NUMBER: 60/413,549
;  PRIOR FILING DATE: 2002-09-25
;  NUMBER OF SEQ ID NOS: 1809
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 507
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-507

  Query Match             61.0%;  Score 12.2;  DB 19;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 2.4e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 TCTTGCAGGAAGCGGCT 20
              || |||| |||| ||||
Db         20 TCCTGCACGAAGTGGCT 4


RESULT 34
US-10-671-395-692/c
; Sequence 692, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Gierse, James K
;  TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: 1179/1/US
;  CURRENT APPLICATION NUMBER: US/10/671,395
;  CURRENT FILING DATE:  2003-09-25
;  PRIOR APPLICATION NUMBER: 60/413,549
;  PRIOR FILING DATE: 2002-09-25
;  NUMBER OF SEQ ID NOS: 1809
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 692
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-692

  Query Match             61.0%;  Score 12.2;  DB 19;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 2.4e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 TCTTGCAGGAAGCGGCT 20
              || |||| |||| ||||
Db         19 TCCTGCACGAAGTGGCT 3


RESULT 35
US-10-719-900-383106/c
; Sequence 383106, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;  FILE REFERENCE: 3528.1
;  CURRENT APPLICATION NUMBER: US/10/719,900
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: 60/427,808
;  PRIOR FILING DATE: 2002 11 20
;  NUMBER OF SEQ ID NOS: 982914
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 383106
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-719-900-383106

  Query Match             61.0%;  Score 12.2;  DB 21;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 2.4e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 CTCTTGCAGGAAGCGGC 19
              ||| || |||||| |||
Db         19 CTCATGTAGGAAGTGGC 3


RESULT 36
US-10-719-956-271624/c
; Sequence 271624, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Rat
;  FILE REFERENCE: 3527.1
;  CURRENT APPLICATION NUMBER: US/10/719,956
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: 60/427,836
;  PRIOR FILING DATE: 2002 11 20
;  NUMBER OF SEQ ID NOS: 699466
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 271624
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-10-719-956-271624

  Query Match             61.0%;  Score 12.2;  DB 22;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 2.4e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 CTCTTGCAGGAAGCGGC 19
              ||| || |||||| |||
Db         19 CTCATGTAGGAAGTGGC 3


RESULT 37
US-10-349-143-8500/c
; Sequence 8500, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
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;  CURRENT APPLICATION NUMBER: US/10/349,143
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: US/09/422,978
;  PRIOR FILING DATE: 1999-10-20
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 8500
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..20
;   OTHER INFORMATION: downstream amplification primer 99-15968 for SEQ 635, in compleme
US-10-349-143-8500

  Query Match             60.0%;  Score 12;  DB 17;  Length 20;
  Best Local Similarity   75.0%;  Pred. No. 3e+04;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GACTCTTGCAGGAAGCGGCT 20
              |||| |||||  |||| | |
Db         20 GACTTTTGCACTAAGCAGAT 1


RESULT 38
US-09-780-533A-91/c
; Sequence 91, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Blatt, Larry
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Chowrira, Bharat
;  APPLICANT:  Haeberli, Pete
;  TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
;  FILE REFERENCE: MBHB00,878-A (400/011)
;  CURRENT APPLICATION NUMBER: US/09/780,533A
;  CURRENT FILING DATE:  2001-02-09
;  PRIOR APPLICATION NUMBER: US 60/181,797
;  PRIOR FILING DATE: 2000-02-11
;  NUMBER OF SEQ ID NOS: 6679
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 91
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-780-533A-91

  Query Match             59.0%;  Score 11.8;  DB 10;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 3.8e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 TTGCAGGAAGCGGCT 20
              ||| | |||||||||
Db         16 TTGAAAGAAGCGGCT 2


RESULT 39
US-09-780-533A-92/c
; Sequence 92, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Blatt, Larry
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Chowrira, Bharat
;  APPLICANT:  Haeberli, Pete
;  TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
;  FILE REFERENCE: MBHB00,878-A (400/011)
;  CURRENT APPLICATION NUMBER: US/09/780,533A
;  CURRENT FILING DATE:  2001-02-09
;  PRIOR APPLICATION NUMBER: US 60/181,797
;  PRIOR FILING DATE: 2000-02-11
;  NUMBER OF SEQ ID NOS: 6679
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 92
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-780-533A-92

  Query Match             59.0%;  Score 11.8;  DB 10;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 3.8e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 TTGCAGGAAGCGGCT 20
              ||| | |||||||||
Db         15 TTGAAAGAAGCGGCT 1


RESULT 40
US-09-780-533A-997/c
; Sequence 997, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Blatt, Larry
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Chowrira, Bharat
;  APPLICANT:  Haeberli, Pete
;  TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
;  FILE REFERENCE: MBHB00,878-A (400/011)
;  CURRENT APPLICATION NUMBER: US/09/780,533A
;  CURRENT FILING DATE:  2001-02-09
;  PRIOR APPLICATION NUMBER: US 60/181,797
;  PRIOR FILING DATE: 2000-02-11
;  NUMBER OF SEQ ID NOS: 6679
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 997
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-780-533A-997

  Query Match             59.0%;  Score 11.8;  DB 10;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 3.8e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 TTGCAGGAAGCGGCT 20
              ||| | |||||||||
Db         17 TTGAAAGAAGCGGCT 3


Search completed: August  6, 2005, 16:35:48
Job time : 342 secs
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OM nucleic - nucleic search, using sw model

Run on: August 6, 2005, 13:40:42 ; Search time 1623 Seconds
(without alignments)
469.061 Million cell updates/sec

Title: US-10-773-678-342
Perfect score: 20
Sequence: 1 gactcttgcaggaagcggct 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 12452

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	10.6	53.0	20	8	AZ314365	AZ314365 1M0031G07
c	2	10.4	52.0	18	1	AJ650912	AJ650912 AJ650912
c	3	10.2	51.0	19	6	CD532073	CD532073 13I04 Ara
c	4	10.2	51.0	20	8	AZ637794	AZ637794 1M0497D20
c	5	9.6	48.0	20	8	AZ336487	AZ336487 1M0066J13
c	6	9.4	47.0	19	8	AZ410317	AZ410317 1M0182L02
	7	9.4	47.0	19	8	AZ816318	AZ816318 2M0085E05
c	8	9.4	47.0	20	8	AZ798282	AZ798282 2M0055H05
	9	9	45.0	19	8	AZ482658	AZ482658 1M0307L16
	10	9	45.0	19	9	CL661094	CL661094 PRI0138d_
	11	9	45.0	20	5	BX559186	BX559186 BX559186
c	12	8.8	44.0	16	5	BQ587767	BQ587767 E012340w-
c	13	8.8	44.0	19	8	AZ481008	AZ481008 1M0302N15
c	14	8.8	44.0	19	8	AZ959942	AZ959942 2M0227L13
c	15	8.6	43.0	20	9	AJ599745	AJ599745 Arabidops
	16	8.4	42.0	16	9	AJ587896	AJ587896 Arabidops
c	17	8.4	42.0	19	8	AZ397615	AZ397615 1M0162M07
c	18	8.4	42.0	19	8	AZ413661	AZ413661 1M0197I07
	19	8.4	42.0	19	8	AZ759607	AZ759607 1M0552I23
	20	8.4	42.0	20	8	AZ597307	AZ597307 1M0410N24
	21	8.4	42.0	20	8	AZ827842	AZ827842 2M0104F03
c	22	8.4	42.0	20	9	AG189193	AG189193 Pan trogl
	23	8.2	41.0	13	5	BQ789829	BQ789829 hage002aH
	24	8.2	41.0	18	1	AI042533	AI042533 oy06e03.x
	25	8.2	41.0	18	6	C00629	C00629 HUMGS000817
	26	8.2	41.0	18	9	CL661466	CL661466 PRI0139d_
	27	8.2	41.0	19	1	AJ666428	AJ666428 AJ666428
	28	8.2	41.0	19	5	BQ587387	BQ587387 S014305-0
	29	8.2	41.0	19	8	AZ363824	AZ363824 1M0109P06
c	30	8.2	41.0	19	8	AZ422762	AZ422762 1M0201P12
	31	8.2	41.0	19	8	AZ509071	AZ509071 1M0351A21
	32	8.2	41.0	19	8	AZ626779	AZ626779 1M0467A14
	33	8.2	41.0	20	8	AZ410583	AZ410583 1M0182B24
c	34	8.2	41.0	20	9	TA207B03Q	AL475823 T. brucei
c	35	8	40.0	19	1	AA916934	AA916934 on14a09.s
c	36	8	40.0	19	3	CNS09MAX	BX064981 Single re
	37	8	40.0	19	8	AZ500630	AZ500630 1M0339A10
c	38	8	40.0	19	8	AZ814554	AZ814554 2M0082P13
	39	8	40.0	20	7	CF305590	CF305590 HDA1--01-
	40	8	40.0	20	8	AZ366451	AZ366451 1M0115N07
	41	8	40.0	20	8	AZ436762	AZ436762 1M0224G12
c	42	8	40.0	20	8	AZ491509	AZ491509 1M0325B09
c	43	8	40.0	20	8	AZ625776	AZ625776 1M0465C08
c	44	8	40.0	20	8	AZ638950	AZ638950 1M0499E08
c	45	8	40.0	20	8	AZ861324	AZ861324 2M0167A13
c	46	7.8	39.0	15	1	AJ665863	AJ665863 AJ665863
	47	7.8	39.0	17	6	CD531254	CD531254 10B19 Ara
c	48	7.8	39.0	17	6	CD533040	CD533040 29N7 Arab
	49	7.8	39.0	17	7	CF305567	CF305567 HDA1--01-
c	50	7.8	39.0	18	9	AJ590049	AJ590049 Arabidops
c	51	7.8	39.0	19	1	AJ660794	AJ660794 AJ660794
c	52	7.8	39.0	19	7	CF318426	CF318426 HD--08-I2
c	53	7.8	39.0	19	8	AZ810098	AZ810098 2M0074N21
c	54	7.8	39.0	19	8	AZ824929	AZ824929 2M0099P16
c	55	7.8	39.0	19	8	AZ847888	AZ847888 2M0148G07
	56	7.8	39.0	19	8	AZ959942	AZ959942 2M0227L13
	57	7.8	39.0	20	1	AL039677	AL039677 DKFZp434H
	58	7.8	39.0	20	1	AL045408	AL045408 DKFZp434E
	59	7.8	39.0	20	8	AQ074235	AQ074235 21 pUC8 P
c	60	7.8	39.0	20	8	AZ482160	AZ482160 1M0307G09
c	61	7.8	39.0	20	8	AZ483003	AZ483003 1M0308G19
	62	7.8	39.0	20	8	AZ665334	AZ665334 1M0546A14
c	63	7.8	39.0	20	8	AZ779169	AZ779169 2M0015N08
	64	7.8	39.0	20	8	AZ787369	AZ787369 2M0033C19
	65	7.8	39.0	20	8	AZ946089	AZ946089 2M0207A13
	66	7.8	39.0	20	8	AZ961140	AZ961140 2M0229P20
	67	7.8	39.0	20	9	AG203570	AG203570 Pan trogl
	68	7.6	38.0	14	9	CL659921	CL659921 PRI0135c_
c	69	7.6	38.0	17	4	BM395339	BM395339 50072-2-8
c	70	7.6	38.0	19	1	AI318366	AI318366 qo53b01.x
	71	7.6	38.0	19	1	AJ657561	AJ657561 AJ657561
c	72	7.6	38.0	19	8	AZ377971	AZ377971 1M0132I03
	73	7.6	38.0	19	8	AZ798955	AZ798955 2M0056K01
c	74	7.6	38.0	19	9	CL436591	CL436591 PST3313-N
c	75	7.6	38.0	20	8	AZ308311	AZ308311 1M0011J12
	76	7.6	38.0	20	8	AZ611227	AZ611227 1M0436E13
	77	7.6	38.0	20	8	AZ775705	AZ775705 2M0008P11
	78	7.6	38.0	20	8	AZ828387	AZ828387 2M0105P13
	79	7.4	37.0	11	9	AJ600625	AJ600625 Arabidops
c	80	7.4	37.0	12	1	AJ648301	AJ648301 AJ648301
c	81	7.4	37.0	15	6	CA851710	CA851710 D16F12_L2
	82	7.4	37.0	16	1	AA881100	AA881100 vz06d08.r
c	83	7.4	37.0	16	7	CF920788	CF920788 gmrhRww3-
c	84	7.4	37.0	16	9	AJ595245	AJ595245 Arabidops
c	85	7.4	37.0	17	2	AW247673	AW247673 2820207.5
	86	7.4	37.0	17	4	BG927979	BG927979 HNC45-1-G
	87	7.4	37.0	17	5	BQ591885	BQ591885 E012580-0
	88	7.4	37.0	17	9	AJ589127	AJ589127 Arabidops
c	89	7.4	37.0	18	5	BQ586080	BQ586080 E012394-0
c	90	7.4	37.0	18	6	CA853355	CA853355 B07C12.se
	91	7.4	37.0	19	1	AI663799	AI663799 uj06a10.x
c	92	7.4	37.0	19	3	CNS08V6Z	BX029847 Single re
c	93	7.4	37.0	19	7	CK576562	CK576562 IST_WI5_1
c	94	7.4	37.0	19	8	AZ314110	AZ314110 1M0030E16
c	95	7.4	37.0	19	8	AZ794653	AZ794653 2M0048G05
c	96	7.4	37.0	19	8	AZ804026	AZ804026 2M0064O07
	97	7.4	37.0	19	8	AZ828745	AZ828745 2M0105J19

c 98	7.4	37.0	20	2	AW246466	AW246466	2821777.3
99	7.4	37.0	20	7	CF339443	CF339443	RCL1--04-
100	7.4	37.0	20	7	CF921355	CF921355	gmrhRww3-

ALIGNMENTS

RESULT 1
AZ314365/c
LOCUS AZ314365 20 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0031G07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0031G07 F, genomic survey sequence.
ACCESSION AZ314365
VERSION AZ314365.1 GI:10360181
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0031 row: G column: 07
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0031G07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
ORIGIN

Query Match 53.0%; Score 10.6; DB 8; Length 20;
Best Local Similarity 76.5%; Pred. No. 1.6e+06;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy          4 TCTTGCAGGAAGCGGCT 20
              || | |||||||| | |
Db         20 TCCTCCAGGAAGCAGGT 4
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RESULT 2
AJ650912/c
LOCUS AJ650912 18 bp mRNA linear EST 07-JUL-2004
DEFINITION AJ650912 CSEQRAN19 Sus scrofa cDNA clone C0003276_L01, mRNA sequence.
ACCESSION AJ650912
VERSION AJ650912.1 GI:49327757
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 18)
AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
JOURNAL Unpublished (2004)
COMMENT Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options. Vector:pBlueScriptII(KS) R. Site1: EcoRI R. Site2: NotI 5' Seq Primer M13F Normalised library constructed from pooled ovaries. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institite, Roslin, Midlothian, UK, EH25 9PS, www.ark-genomics.org.
FEATURES Location/Qualifiers
source 1. .18
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0003276_L01"
/tissue_type="ovary"
/clone_lib="CSEQRAN19"
/note="Vector: pBlueScriptII(KS+); Site_1: EcoRI; Site_2: NotI; Single pass sequencing; Normalised library constructed from pooled ovaries"
ORIGIN

Query Match 52.0%; Score 10.4; DB 1; Length 18;
Best Local Similarity 91.7%; Pred. No. 2e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          8 GCAGGAAGCGGC 19
              |||| |||||||
Db         12 GCAGCAAGCGGC 1
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RESULT 3
CD532073/c
LOCUS CD532073 19 bp mRNA linear EST 31-DEC-2003
DEFINITION 13I04 Arabidopsis Leaf Senescence Library Arabidopsis thaliana cDNA 3', mRNA sequence.
ACCESSION CD532073
VERSION CD532073.1 GI:40452085
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 19)
AUTHORS Guo,Y., Cai,Z. and Gan,S.

```
  TITLE     Transcriptome of Arabidopsis leaf senescence
  JOURNAL   Plant Cell Environ. 27 (5), 521-549 (2004)
COMMENT     Contact: Susheng Gan
            Department of Horticulture
            Cornell University
            119 Plant Science, Cornell University, Ithaca, NY 14853-5904, USA
            Tel: 607 254 5418
            Fax: 607 255 0599
            Email: sg288@cornell.edu
            Insert Length: 19   Std Error: 0.00
            Seq primer: T7
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Arabidopsis thaliana"
                     /mol_type="mRNA"
                     /ecotype="Landsberg erecta"
                     /db_xref="taxon:3702"
                     /tissue_type="Leaf"
                     /dev_stage="Yellow Leaf With Greenish Base Area"
                     /lab_host="E. coli"
                     /clone_lib="Arabidopsis Leaf Senescence Library"
                     /note="Organ: Rosette Leaf; Vector: pBluscript SKII+;
                     Site_1: EcoRI; Site_2: EcoRI; Senescent rosette leaves #5
                     and #6 (counted from the bottom) were  harvested and
                     immediately frozen in liquid N2. The leaves were  visibly
                     yellow excepted for the leaf base areas that were still
                     greenish. "
ORIGIN

  Query Match             51.0%;  Score 10.2;  DB 6;  Length 19;
  Best Local Similarity   80.0%;  Pred. No. 2.6e+06;
  Matches   12;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 CTTGCAGGAAGCGGC 19
              | || ||||||| ||
Db         19 CGTGAAGGAAGCAGC 5


RESULT 4
AZ637794/c
LOCUS       AZ637794                 20 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0497D20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0497D20 F, genomic survey sequence.
ACCESSION   AZ637794
VERSION     AZ637794.1  GI:11759984
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0497  row: D  column: 20
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0497D20"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             51.0%;  Score 10.2;  DB 8;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 2.6e+06;
  Matches   12;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GACTCTTGCAGGAAG 15
              | ||||| |||| |
Db         16 GGCTCTTGGAGGAGG 2


RESULT 5
AZ336487/c
LOCUS       AZ336487                 20 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0066J13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0066J13 R, genomic survey sequence.
ACCESSION   AZ336487
VERSION     AZ336487.1  GI:10405834
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0066  row: J  column: 13
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
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    source          1. .20
                    /organism="Mus musculus"
                    /mol_type="genomic DNA"
                    /strain="C57BL/6J"
                    /db_xref="taxon:10090"
                    /clone="UUGC1M0066J13"
                    /sex="Male"
                    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                    /clone_lib="Mouse 10kb plasmid UUGC1M library"
                    /note="Vector: PWD42nv; Purified genomic DNA from M.
                    musculus C57BL/6J (male) was obtained  from the Jackson
                    Laboratory Mouse DNA Resource
                    (http://www.jax.org/resources/documents/dnares/). The DNA
                    was hydrodynamically sheared by repeated passage through a
                    0.005 inch orifice at constant velocity. The sheared DNA
                    was blunt end-repaired with T4 DNA polymerase and T4
                    polynucleotide kinase. Adaptor oligonucleotides were
                    ligated to the blunt ends in high  molar excess. The
                    adaptored DNA was purified and size-selected for a 9.5 to
                    10.5 kb range using preparative agarose gel
                    electrophoresis. Vector DNA was prepared from a derivative
                    of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                    inducible derivative of plasmid R1. The vector was ligated
                    with adaptors complementary to the insert adaptors and
                    purified. The sheared, adaptored mouse DNA was annealed to
                    adaptored vector DNA, and transformed into
                    chemically-competent E. coli XL10-Gold (Stratagene) cells
                    and selected for ampicillin resistance."
ORIGIN

  Query Match             48.0%;  Score 9.6;  DB 8;  Length 20;
  Best Local Similarity   75.0%;  Pred. No. 5.1e+06;
  Matches   12;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 ACTCTTGCAGGAAGCG 17
              ||| |||||||  | |
Db         17 ACTGTTGCAGGGTGGG 2


RESULT 6
AZ410317/c
LOCUS       AZ410317                 19 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0182L02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0182L02 R, genomic survey sequence.
ACCESSION   AZ410317
VERSION     AZ410317.1  GI:10534330
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0182  row: L  column: 02
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
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                    /organism="Mus musculus"
                    /mol_type="genomic DNA"
                    /strain="C57BL/6J"
                    /db_xref="taxon:10090"
                    /clone="UUGC1M0182L02"
                    /sex="Male"
                    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                    /clone_lib="Mouse 10kb plasmid UUGC1M library"
                    /note="Vector: PWD42nv; Purified genomic DNA from M.
                    musculus C57BL/6J (male) was obtained  from the Jackson
                    Laboratory Mouse DNA Resource
                    (http://www.jax.org/resources/documents/dnares/). The DNA
                    was hydrodynamically sheared by repeated passage through a
                    0.005 inch orifice at constant velocity. The sheared DNA
                    was blunt end-repaired with T4 DNA polymerase and T4
                    polynucleotide kinase. Adaptor oligonucleotides were
                    ligated to the blunt ends in high  molar excess. The
                    adaptored DNA was purified and size-selected for a 9.5 to
                    10.5 kb range using preparative agarose gel
                    electrophoresis. Vector DNA was prepared from a derivative
                    of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                    inducible derivative of plasmid R1. The vector was ligated
                    with adaptors complementary to the insert adaptors and
                    purified. The sheared, adaptored mouse DNA was annealed to
                    adaptored vector DNA, and transformed into
                    chemically-competent E. coli XL10-Gold (Stratagene) cells
                    and selected for ampicillin resistance."
ORIGIN

  Query Match             47.0%;  Score 9.4;  DB 8;  Length 19;
  Best Local Similarity   90.9%;  Pred. No. 6.3e+06;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 TTGCAGGAAGC 16
              ||||| |||||
Db         16 TTGCAAGAAGC 6


RESULT 7
AZ816318
LOCUS       AZ816318                 19 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0085E05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0085E05 F, genomic survey sequence.
ACCESSION   AZ816318
VERSION     AZ816318.1  GI:12986226
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0085  row: E  column: 05
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
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                    /organism="Mus musculus"
                    /mol_type="genomic DNA"
                    /strain="C57BL/6J"
                    /db_xref="taxon:10090"
                    /clone="UUGC2M0085E05"
                    /sex="Male"
                    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                    /clone_lib="Mouse 10kb plasmid UUGC1M library"
                    /note="Vector: PWD42nv; Purified genomic DNA from M.
                    musculus C57BL/6J (male) was obtained  from the Jackson
                    Laboratory Mouse DNA Resource
                    (http://www.jax.org/resources/documents/dnares/). The DNA
                    was hydrodynamically sheared by repeated passage through a
                    0.005 inch orifice at constant velocity. The sheared DNA
                    was blunt end-repaired with T4 DNA polymerase and T4
                    polynucleotide kinase. Adaptor oligonucleotides were
                    ligated to the blunt ends in high  molar excess. The
                    adaptored DNA was purified and size-selected for a 9.5 to
                    10.5 kb range using preparative agarose gel
                    electrophoresis. Vector DNA was prepared from a derivative
                    of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                    inducible derivative of plasmid R1. The vector was ligated
                    with adaptors complementary to the insert adaptors and
                    purified. The sheared, adaptored mouse DNA was annealed to
                    adaptored vector DNA, and transformed into
                    chemically-competent E. coli XL10-Gold (Stratagene) cells
                    and selected for ampicillin resistance."
ORIGIN

  Query Match             47.0%;  Score 9.4;  DB 8;  Length 19;
  Best Local Similarity   90.9%;  Pred. No. 6.3e+06;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 AGGAAGCGGCT 20
              ||||| |||||
Db          2 AGGAAACGGCT 12


RESULT 8
AZ798282/c
LOCUS       AZ798282                 20 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0055H05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0055H05 F, genomic survey sequence.
ACCESSION   AZ798282
VERSION     AZ798282.1  GI:12948227
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0055  row: H  column: 05
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
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    source          1. .20
                    /organism="Mus musculus"
                    /mol_type="genomic DNA"
                    /strain="C57BL/6J"
                    /db_xref="taxon:10090"
                    /clone="UUGC2M0055H05"
                    /sex="Male"
                    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                    /clone_lib="Mouse 10kb plasmid UUGC1M library"
                    /note="Vector: PWD42nv; Purified genomic DNA from M.
                    musculus C57BL/6J (male) was obtained  from the Jackson
                    Laboratory Mouse DNA Resource
                    (http://www.jax.org/resources/documents/dnares/). The DNA
                    was hydrodynamically sheared by repeated passage through a
                    0.005 inch orifice at constant velocity. The sheared DNA
                    was blunt end-repaired with T4 DNA polymerase and T4
                    polynucleotide kinase. Adaptor oligonucleotides were
                    ligated to the blunt ends in high  molar excess. The
                    adaptored DNA was purified and size-selected for a 9.5 to
                    10.5 kb range using preparative agarose gel
                    electrophoresis. Vector DNA was prepared from a derivative
                    of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                    inducible derivative of plasmid R1. The vector was ligated
                    with adaptors complementary to the insert adaptors and
                    purified. The sheared, adaptored mouse DNA was annealed to
                    adaptored vector DNA, and transformed into
                    chemically-competent E. coli XL10-Gold (Stratagene) cells
                    and selected for ampicillin resistance."
ORIGIN

  Query Match             47.0%;  Score 9.4;  DB 8;  Length 20;
  Best Local Similarity   90.9%;  Pred. No. 6.4e+06;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 ACTCTTGCAGG 12
              ||||||||| |
Db         16 ACTCTTGCATG 6


RESULT 9
AZ482658
LOCUS       AZ482658                 19 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0307L16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0307L16 R, genomic survey sequence.
ACCESSION   AZ482658
VERSION     AZ482658.1  GI:10645919
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0307  row: L  column: 16
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
```

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    source          1. .19
                    /organism="Mus musculus"
                    /mol_type="genomic DNA"
                    /strain="C57BL/6J"
                    /db_xref="taxon:10090"
                    /clone="UUGC1M0307L16"
                    /sex="Male"
                    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                    /clone_lib="Mouse 10kb plasmid UUGC1M library"
                    /note="Vector: PWD42nv; Purified genomic DNA from M.
                    musculus C57BL/6J (male) was obtained  from the Jackson
                    Laboratory Mouse DNA Resource
                    (http://www.jax.org/resources/documents/dnares/). The DNA
                    was hydrodynamically sheared by repeated passage through a
                    0.005 inch orifice at constant velocity. The sheared DNA
                    was blunt end-repaired with T4 DNA polymerase and T4
                    polynucleotide kinase. Adaptor oligonucleotides were
                    ligated to the blunt ends in high  molar excess. The
                    adaptored DNA was purified and size-selected for a 9.5 to
                    10.5 kb range using preparative agarose gel
                    electrophoresis. Vector DNA was prepared from a derivative
                    of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                    inducible derivative of plasmid R1. The vector was ligated
                    with adaptors complementary to the insert adaptors and
                    purified. The sheared, adaptored mouse DNA was annealed to
                    adaptored vector DNA, and transformed into
                    chemically-competent E. coli XL10-Gold (Stratagene) cells
                    and selected for ampicillin resistance."
ORIGIN

  Query Match             45.0%;  Score 9;  DB 8;  Length 19;
  Best Local Similarity   70.6%;  Pred. No. 9.9e+06;
  Matches   12;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 CTCTTGCAGGAAGCGGC 19
              |||| |||||   | ||
Db          3 CTCTGGCAGGTTACTGC 19


RESULT 10
CL661094
LOCUS       CL661094                19 bp    DNA     linear   GSS 09-JUL-2004
DEFINITION  PRI0138d_F10 - PRI0138d.B21 (19) Mixed stage fosmid library of P.
            pacificus var. California Pristionchus pacificus genomic, genomic
            survey sequence.
ACCESSION   CL661094
VERSION     CL661094.1  GI:50147102
KEYWORDS    GSS.
SOURCE      Pristionchus pacificus
  ORGANISM  Pristionchus pacificus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
            Neodiplogasteridae; Pristionchus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
  TITLE     AppaDB: an AcedB database for the nematode satellite organism
            Pristionchus pacificus
  JOURNAL   Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT     Contact: Sommer RJ
            Evolutionary Biology
            Max-Planck-Institute for Developmental Biology
            Spemannstr. 37-39, Tuebingen D-72076, Germany
            Tel: 00497071601371
            Fax: 00497071601498
            Email: ralf.sommer@tuebingen.mpg.de
            This library was generated at Caltech, Pasadena, USA and end
            sequenced at Vancouver, Canada.
            Seq primer: T7
            Class: fosmid ends.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Pristionchus pacificus"
                     /mol_type="genomic DNA"
                     /strain="California"
                     /db_xref="taxon:54126"
                     /clone_lib="Mixed stage fosmid library of P. pacificus
                     var. California"
                     /note="Vector: pEpifos-5 Fosmid vector"
ORIGIN

  Query Match             45.0%;  Score 9;  DB 9;  Length 19;
  Best Local Similarity   70.6%;  Pred. No. 9.9e+06;
  Matches   12;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          4 TCTTGCAGGAAGCGGCT 20
              ||| | || ||  ||||
Db          1 TCTCGTAGCAAAAGGCT 17


RESULT 11
BX559186
LOCUS       BX559186                20 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX559186 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse42b02_q1c, mRNA sequence.
ACCESSION   BX559186
VERSION     BX559186.1  GI:33366480
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse42b02_q1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"
ORIGIN

  Query Match             45.0%;  Score 9;  DB 5;  Length 20;
  Best Local Similarity   70.6%;  Pred. No. 1e+07;
  Matches   12;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 CTCTTGCAGGAAGCGGC 19
              |||| | | |||| | |
Db          3 CTCTAGTAAGAAGTGAC 19


RESULT 12
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BQ587767/c
LOCUS       BQ587767                  16 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012340w-024-010-M01-SP6 MPIZ-ADIS-024-leaf Beta vulgaris cDNA
            clone 024-010-M01 5-PRIME, mRNA sequence.
ACCESSION   BQ587767
VERSION     BQ587767.1  GI:26117349
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 16   Std Error: 0.00
            Plate: 10  row: M  column: 01
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:185096"
                     /db_xref="taxon:161934"
                     /clone="024-010-M01"
                     /tissue_type="leaf"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-leaf"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database:http://gabi.rzpd.de"
ORIGIN

  Query Match             44.0%;  Score 8.8;  DB 5;  Length 16;
  Best Local Similarity   83.3%;  Pred. No. 1.2e+07;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 TTGCAGGAAGCG 17
              |||||||| | |
Db         16 TTGCAGGAGGAG 5


RESULT 13
AZ481008/c
LOCUS       AZ481008                  19 bp    DNA     linear   GSS 04-OCT-2000
DEFINITION  1M0302N15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0302N15 R, genomic survey sequence.
ACCESSION   AZ481008
VERSION     AZ481008.1  GI:10641989
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0302  row: N  column: 15
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0302N15"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             44.0%;  Score 8.8;  DB 8;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 1.2e+07;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          9 CAGGAAGCGGCT 20
              ||| |||| |||
Db         18 CAGAAAGCAGCT 7


RESULT 14
AZ959942/c
LOCUS       AZ959942                  19 bp    DNA     linear   GSS 27-APR-2001
DEFINITION  2M0227L13R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
            clone UUGC2M0227L13 R, genomic survey sequence.
ACCESSION   AZ959942
VERSION     AZ959942.1  GI:13831169
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
```

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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0227  row: L  column: 13
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0227L13"
                     /sex="Female"
                     /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC2M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (female) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             44.0%;  Score 8.8;  DB 8;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 1.2e+07;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 TCTTGCAGGAAG 15
              | ||||||  |||
Db         13 TATTGCAGCAAG 2


RESULT 15
AJ599745/c
LOCUS       AJ599745                 20 bp    DNA     linear   GSS 15-JAN-2004
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, left border, clone
            492G09, genomic survey sequence.
ACCESSION   AJ599745
VERSION     AJ599745.1  GI:37949373
KEYWORDS    GSS; left border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
  TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
  JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
  MEDLINE   22363535
   PUBMED   12446565
REFERENCE   2  (bases 1 to 20)
  AUTHORS   Balzergue,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Wassillewskija"
                     /db_xref="taxon:3702"
                     /clone="492G09"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature    1. .20
                     /note="T-DNA flanking sequence
                     left border"
ORIGIN

  Query Match             43.0%;  Score 8.6;  DB 9;  Length 20;
  Best Local Similarity   73.3%;  Pred. No. 1.6e+07;
  Matches   11;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 ACTCTTGCAGGAAGC 16
              ||| || |  |||||
Db         17 ACTGTTTCCAGAAGC 3


RESULT 16
AJ587896
LOCUS       AJ587896                 16 bp    DNA     linear   GSS 15-JAN-2004
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, left border, clone
            337H10, genomic survey sequence.
ACCESSION   AJ587896
VERSION     AJ587896.1  GI:37937520
KEYWORDS    GSS; left border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
  TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
  JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
  MEDLINE   22363535
   PUBMED   12446565
REFERENCE   2  (bases 1 to 16)
```

```
  AUTHORS   Balzergue,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Wassillewskija"
                     /db_xref="taxon:3702"
                     /clone="337H10"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature    1. .16
                     /note="T-DNA flanking sequence
                     left border"
ORIGIN

  Query Match             42.0%;  Score 8.4;  DB 9;  Length 16;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+07;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TCTTGCAGGA 13
              |||||||| |
Db          3 TCTTGCAGTA 12


RESULT 17
AZ397615/c
LOCUS       AZ397615                 19 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0162M07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0162M07 R, genomic survey sequence.
ACCESSION   AZ397615
VERSION     AZ397615.1  GI:10512687
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0162  row: M  column: 07
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0162M07"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             42.0%;  Score 8.4;  DB 8;  Length 19;
  Best Local Similarity   90.0%;  Pred. No. 2e+07;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 TTGCAGGAAG 15
              || |||||||
Db         11 TTACAGGAAG 2


RESULT 18
AZ413661/c
LOCUS       AZ413661                 19 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0197I07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0197I07 R, genomic survey sequence.
ACCESSION   AZ413661
VERSION     AZ413661.1  GI:10537590
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0197  row: I  column: 07
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
```

/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0197I07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 42.0%; Score 8.4; DB 8; Length 19;
Best Local Similarity 90.0%; Pred. No. 2e+07;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 GACTCTTGCA 10
              ||| ||||||
Db         10 GACCCTTGCA 1
```

RESULT 19
AZ759607
LOCUS AZ759607 19 bp DNA linear GSS 16-FEB-2001
DEFINITION 1M0552I23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0552I23 F, genomic survey sequence.
ACCESSION AZ759607
VERSION AZ759607.1 GI:12866570
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0552 row: I column: 23
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0552I23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 42.0%; Score 8.4; DB 8; Length 19;
Best Local Similarity 90.0%; Pred. No. 2e+07;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          7 TGCAGGAAGC 16
              ||||||| ||
Db          9 TGCAGGATGC 18
```

RESULT 20
AZ597307
LOCUS AZ597307 20 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0410N24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0410N24 R, genomic survey sequence.
ACCESSION AZ597307
VERSION AZ597307.1 GI:11719413
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0410 row: N column: 24
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"

/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0410N24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 42.0%; Score 8.4; DB 8; Length 20;
Best Local Similarity 90.0%; Pred. No. 2e+07;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CTCTTGCAGG 12
||||||||| |
Db 7 CTCTTGCATG 16

RESULT 21
AZ827842
LOCUS AZ827842 20 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0104F03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0104F03 R, genomic survey sequence.
ACCESSION AZ827842
VERSION AZ827842.1 GI:12997750
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0104 row: F column: 03
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0104F03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 42.0%; Score 8.4; DB 8; Length 20;
Best Local Similarity 66.7%; Pred. No. 2e+07;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 CTCTTGCAGGAAGCGGCT 20
|| | ||| ||| | ||
Db 3 CTGTGGCAAGAAACATCT 20

RESULT 22
AG189193/c
LOCUS AG189193 20 bp DNA linear GSS 06-MAR-2004
DEFINITION Pan troglodytes DNA, clone: RP43-063J03.T7, genomic survey sequence.
ACCESSION AG189193
VERSION AG189193.1 GI:45221369
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1
AUTHORS Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J., Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
TITLE BAC end sequences of Library RP-43
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 20)
AUTHORS Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J., Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
TITLE Direct Submission
JOURNAL Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC); 52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea (E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/, Tel:82-42-866-7181, Fax:82-42-860-4409)
COMMENT Clones are derived from the chimpanzee BAC library RP-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
PRIMERS
Sequencing: T7
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
FEATURES Location/Qualifiers

```
     source          1. .20
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
                     /clone="RP43-063J03.T7"
                     /sex="male"
                     /cell_type="lymphocytes"
                     /clone_lib="RP-43 Chimpanzee Male BAC Library"
ORIGIN

  Query Match             42.0%;  Score 8.4;  DB 9;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2e+07;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 TTGCAGGAAG 15
              ||||||| ||
Db         10 TTGCAGGGAG 1


RESULT 23
BQ789829
LOCUS       BQ789829                 13 bp    mRNA    linear   EST 30-JUL-2002
DEFINITION  hage002aH08 Heterobasidion annosum - Scots pine infection stage
            (HAGE) subtraction cDNA library Pinus sylvestris/Heterobasidion
            annosum mixed EST library cDNA clone hage002aH08, mRNA sequence.
ACCESSION   BQ789829
VERSION     BQ789829.1  GI:22004791
KEYWORDS    EST.
SOURCE      Pinus sylvestris/Heterobasidion annosum mixed EST library
  ORGANISM  Pinus sylvestris/Heterobasidion annosum mixed EST library
            Eukaryota; mixed EST libraries.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Asiegbu,F.O., Nahalkova,J. and Dean,R.A.
  TITLE     Selected Expressed sequence tags of cDNA clones from the
            interaction of the root rot fungus (Heterobasidion annosum) with
            seedling roots of Scots pine (Pinus sylvestris)
  JOURNAL   Unpublished (2C01)
COMMENT     Contact: Fred O. Asiegbu
            Dept. of Forest Mycology & Pathology
            Swedish University of Agriculture, Box 7026,S-750 07, Uppsala,
            Sweden
            Tel: +46 18 67 15 98
            Fax: +46 18 30 92 45
            Email: Fred.Asiegbu@mykopat.slu.se
            Seq primer: T7 primer.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Pinus sylvestris/Heterobasidion annosum mixed
                     EST library"
                     /mol_type="mRNA"
                     /db_xref="taxon:169015"
                     /clone="hage002aH08"
                     /dev_stage="Seedling roots of scots pine were infected for
                     6 days with H. annosum"
                     /clone_lib="Heterobasidion annosum - Scots pine infection
                     stage (HAGE) subtraction cDNA library"
                     /note="Vector: pT-Adv; Site_1: EcoRI; The subtractive
                     hybridization cDNA library was constructed from scots pine
                     roots infected for 6-days with mycelia of Heterobasidon
                     annosum (FP5)."
ORIGIN

  Query Match             41.0%;  Score 8.2;  DB 5;  Length 13;
  Best Local Similarity   76.9%;  Pred. No. 2.3e+07;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 CTCTTGCAGGAAG 15
              ||||| ||| | |
Db          1 CTCTTACAGCATG 13


RESULT 24
AI042533
LOCUS       AI042533                 18 bp    mRNA    linear   EST 30-JUN-1998
DEFINITION  oy06e03.x1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA
            clone IMAGE:1665052 3' similar to TR:Q15662 Q15662
            TRANSFORMATION-RELATED PROTEIN ;, mRNA sequence.
ACCESSION   AI042533
VERSION     AI042533.1  GI:3281727
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1665052"
                     /tissue_type="senescent fibroblast"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares_senescent_fibroblasts_NbHSF"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco
                     RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                     primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo."
ORIGIN

  Query Match             41.0%;  Score 8.2;  DB 1;  Length 18;
  Best Local Similarity   76.9%;  Pred. No. 2.4e+07;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GACTCTTGCAGGA 13
              ||| || | ||||
Db          6 GACACTGGAAGGA 18


RESULT 25
C00629
LOCUS       C00629                   18 bp    mRNA    linear   EST 31-DEC-2002
DEFINITION  HUMGS0008172 Human adult (K.Okubo) Homo sapiens cDNA, mRNA
            sequence.
ACCESSION   C00629
VERSION     C00629.1  GI:1432859
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Okubo,K.
  TITLE     BodyMap; human gene expression database
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Okubo,K.
            Institute for Molecular and Cellular Biol
            Osaka University
```

```
            1-3,Yamada-oka, Suita, Osaka Pref. 565, Japan
            Tel: 06-877-5111(ex.3315)
            Email: kousaku@imcb.osaka-u.ac.jp
            We are not submitting the same cDNA sequence redundantly to DDBJ
            since 1993. For the abundance information of clones with this
            sequence in this library and as well as in other 3'-directed
            libraries, see ' http://www.imcb.osaka- u.ac.jp/bodymap'. The
            sequences of the clones represented by this GS sequences is also
            found there.
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /dev_stage="adult"
                      /clone_lib="Human adult (K.Okubo)"
                      /note="One or more human adult tissue"
ORIGIN

  Query Match             41.0%;  Score 8.2;  DB 6;  Length 18;
  Best Local Similarity   76.9%;  Pred. No. 2.4e+07;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 TCTTGCAGGAAGC 16
              |||||| | || |
Db          3 TCTTGCTGAAAAC 15


RESULT 26
CL661466
LOCUS       CL661466                 18 bp    DNA     linear   GSS 09-JUL-2004
DEFINITION  PRI0139d_G02 - PRI0139d.B21 (18) Mixed stage fosmid library of P.
            pacificus var. California Pristionchus pacificus genomic, genomic
            survey sequence.
ACCESSION   CL661466
VERSION     CL661466.1  GI:50147979
KEYWORDS    GSS.
SOURCE      Pristionchus pacificus
  ORGANISM  Pristionchus pacificus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
            Neodiplogasteridae; Pristionchus.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
  TITLE     AppaDB: an AcedB database for the nematode satellite organism
            Pristionchus pacificus
  JOURNAL   Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT     Contact: Sommer RJ
            Evolutionary Biology
            Max-Planck-Institute for Developmental Biology
            Spemannstr. 37-39, Tuebingen D-72076, Germany
            Tel: 00497071601371
            Fax: 00497071601498
            Email: ralf.sommer@tuebingen.mpg.de
            This library was generated at Caltech, Pasadena, USA and end
            sequenced at Vancouver, Canada.
            Seq primer: T7
            Class: fosmid ends.
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="Pristionchus pacificus"
                      /mol_type="genomic DNA"
                      /strain="California"
                      /db_xref="taxon:54126"
                      /clone_lib="Mixed stage fosmid library of P. pacificus
                      var. California"
                      /note="Vector: pEpifos-5 Fosmid vector"
ORIGIN

  Query Match             41.0%;  Score 8.2;  DB 9;  Length 18;
  Best Local Similarity   76.9%;  Pred. No. 2.4e+07;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GACTCTTGCAGGA 13
              || |||| | |||
Db          2 GAATCTTTCTGGA 14


RESULT 27
AJ666428
LOCUS       AJ666428                 19 bp    mRNA    linear   EST 28-JUN-2004
DEFINITION  AJ666428 CSEQRAN09 Sus scrofa cDNA clone C0000033_N10, mRNA
            sequence.
ACCESSION   AJ666428
VERSION     AJ666428.1  GI:49350879
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
  TITLE     Development of cDNA and EST resources for studying reproduction and
            embryo development in pigs and cattle
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Anderson SI
            Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
            Single pass sequencing. Bases called and trimmed with phred
            v0.020425.c. Vector identified by cross_match with the -minscore 20
            and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site 1:
            EcoRI R. Site 2: NotI Description: Normalised library constructed
            from pooled tissue from day 30 placentas. Clones available from UK
            Centre for Functional Genomics in Farm Animals, Roslin Institite,
            Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="Sus scrofa"
                      /mol_type="mRNA"
                      /db_xref="taxon:9823"
                      /clone="C0000033_N10"
                      /tissue_type="placenta"
                      /clone_lib="CSEQRAN09"
                      /note="Vector: pBlueScriptII(KS+); Site_1: EcoRI; Site_2:
                      NotI; Single pass sequencing. Normalised library
                      constructed from pooled tissue from day 30 placentas."
ORIGIN

  Query Match             41.0%;  Score 8.2;  DB 1;  Length 19;
  Best Local Similarity   76.9%;  Pred. No. 2.4e+07;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          8 GCAGGAAGCGGCT 20
              ||  || ||||||
Db          4 GCTCGAGGCGGCT 16


RESULT 28
BQ587387
LOCUS       BQ587387                 19 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  S014305-024-010-H05-SP6 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone
            024-010-H05 5-PRIME, mRNA sequence.
ACCESSION   BQ587387
VERSION     BQ587387.1  GI:26116969
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide .
            fingerprinting allows access to 25 000 potential sugar beet genes
```

```
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 19   Std Error: 0.00
            Plate: 10  row: H  column: 05
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:185481"
                     /db_xref="taxon:161934"
                     /clone="024-010-H05"
                     /tissue_type="leaf"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-leaf"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database:http://gabi.rzpd.de"
ORIGIN

  Query Match             41.0%;  Score 8.2;  DB 5;  Length 19;
  Best Local Similarity   76.9%;  Pred. No. 2.4e+07;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 CTCTTGCAGGAAG 15
              |||| || | |||
Db          6 CTCTGGCCGCAAG 18


RESULT 29
AZ363824
LOCUS       AZ363824                 19 bp    DNA     linear   GSS 02-OCT-2000
DEFINITION  1M0109P06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0109P06 R, genomic survey sequence.
ACCESSION   AZ363824
VERSION     AZ363824.1  GI:10477524
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0109  row: P  column: 06
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0109P06"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             41.0%;  Score 8.2;  DB 8;  Length 19;
  Best Local Similarity   76.9%;  Pred. No. 2.4e+07;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 CTTGCAGGAAGCG 17
              ||  ||||||| |
Db          1 CTGACAGGAAGTG 13


RESULT 30
AZ422762/c
LOCUS       AZ422762                 19 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0201P12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0201P12 R, genomic survey sequence.
ACCESSION   AZ422762
VERSION     AZ422762.1  GI:10546871
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
```

```
          Insert Length: 10000   Std Error: 0.00
          Plate: 0201  row: P  column: 12
          Seq primer: CACACAGGAAACAGCTATGACC
          Class: plasmid ends
          High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0201P12"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             41.0%;  Score 8.2;  DB 8;  Length 19;
  Best Local Similarity   76.9%;  Pred. No. 2.4e+07;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          6 TTGCAGGAAGCGG 18
              ||||||| |  ||
Db         19 TTGCAGGCACAGG 7


RESULT 31
AZ509071
LOCUS       AZ509071                 19 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0351A21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0351A21 R, genomic survey sequence.
ACCESSION   AZ509071
VERSION     AZ509071.1  GI:10690387
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
```

```
          Insert Length: 10000   Std Error: 0.00
          Plate: 0351  row: A  column: 21
          Seq primer: CACACAGGAAACAGCTATGACC
          Class: plasmid ends
          High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0351A21"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             41.0%;  Score 8.2;  DB 8;  Length 19;
  Best Local Similarity   76.9%;  Pred. No. 2.4e+07;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          7 TGCAGGAAGCGGC 19
              ||| || || |||
Db          1 TGCTGGCAGAGGC 13


RESULT 32
AZ626779
LOCUS       AZ626779                 19 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0467A14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0467A14 F, genomic survey sequence.
ACCESSION   AZ626779
VERSION     AZ626779.1  GI:11748969
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
```

Insert Length: 10000 Std Error: 0.00
Plate: 0467 row: A column: 14
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0467A14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 41.0%; Score 8.2; DB 8; Length 19;
Best Local Similarity 76.9%; Pred. No. 2.4e+07;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CTCTTGCAGGAAG 15
| ||| |||| ||
Db 4 CACTTTCAGGCAG 16

RESULT 33
AZ410583
LOCUS AZ410583 20 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0182E24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0182E24 R, genomic survey sequence.
ACCESSION AZ410583
VERSION AZ410583.1 GI:10534512
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0182 row: E column: 24
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0182E24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 41.0%; Score 8.2; DB 8; Length 20;
Best Local Similarity 76.9%; Pred. No. 2.5e+07;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGA 13
|| |||| ||| |
Db 4 GATTCTTCCAGCA 16

RESULT 34
TA207B03Q/c
LOCUS TA207B03Q 20 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 207b03, reverse sequence, genomic survey sequence.
ACCESSION AL475823
VERSION AL475823.1 GI:11842591
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
REFERENCE 1 (bases 1 to 20)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh1@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In

Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES Location/Qualifiers
source 1. .20
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="207b03"

ORIGIN

Query Match 41.0%; Score 8.2; DB 9; Length 20;
Best Local Similarity 76.9%; Pred. No. 2.5e+07;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGA 13
| ||| ||||| |
Db 19 GTCTCATGCAGCA 7

RESULT 35
AA916934/c
LOCUS AA916934 19 bp mRNA linear EST 17-JUN-1998
DEFINITION on14a09.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1556632 3' similar to SW:BI3_MOUSE P28662 BRAIN PROTEIN I3 ;, mRNA sequence.
ACCESSION AA916934
VERSION AA916934.1 GI:3056326
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 19)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 444 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.

FEATURES Location/Qualifiers
source 1. .19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1556632"
/tissue_type="carcinoid"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Lu5"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 40.0%; Score 8; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.1e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TTGCAGGA 13
||||||||
Db 8 TTGCAGGA 1

RESULT 36
CNS09MAX/c
LOCUS CNS09MAX 19 bp mRNA linear HTC 08-JAN-2003
DEFINITION Single read from an extremity of a full-length cDNA clone made from Anopheles gambiae total adult females. 3-PRIME end of clone FK0AAC48CF12 of strain 6-9 of Anopheles gambiae (African malaria mosquito).
ACCESSION BX064981
VERSION BX064981.1 GI:27638262
KEYWORDS HTC.
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
REFERENCE 1 (bases 1 to 19)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (06-JAN-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

FEATURES Location/Qualifiers
source 1. .19
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="6-9"
/db_xref="taxon:7165"
/clone="FK0AAC48CF12"
/plasmid="pME18S-FL"
/note="end : 3-PRIME"

ORIGIN

Query Match 40.0%; Score 8; DB 3; Length 19;
Best Local Similarity 68.8%; Pred. No. 3.1e+07;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 CTCTTGCAGGAAGCGG 18
| | ||| |||| ||
Db 19 CCCGGGCACGAAGGGG 4

RESULT 37
AZ500630
LOCUS AZ500630 19 bp DNA linear GSS 05-OCT-2000
DEFINITION 1M0339A10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0339A10 F, genomic survey sequence.
ACCESSION AZ500630
VERSION AZ500630.1 GI:10680639
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

```
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0339  row: A  column: 10
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0339A10"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
ORIGIN

  Query Match            40.0%;  Score 8;  DB 8;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 3.1e+07;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 CAGGAAGC 16
              ||||||||
Db          3 CAGGAAGC 10


RESULT 38
AZ814554/c
LOCUS       AZ814554                 19 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0082P13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0082P13 F, genomic survey sequence.
ACCESSION   AZ814554
VERSION     AZ814554.1  GI:12984462
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0082  row: P  column: 13
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC2M0082P13"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
ORIGIN

  Query Match            40.0%;  Score 8;  DB 8;  Length 19;
  Best Local Similarity  68.8%;  Pred. No. 3.1e+07;
  Matches   11;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          4 TCTTGCAGGAAGCGGC 19
              ||   |||||| | ||
Db         16 TCACACAGGAAACAGC 1


RESULT 39
CF305590
LOCUS       CF305590                 20 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HDA1--01-C09.g1 OsHDAC1-overexpressing transgenic rice lambda phage
            cDNA library I (HDA1) Oryza sativa (japonica cultivar-group) cDNA
            clone HDA1--01-C09, mRNA sequence.
ACCESSION   CF305590
VERSION     CF305590.1  GI:33677351
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="Oryza sativa (japonica cultivar-group)"
                      /mol_type="mRNA"
                      /cultivar="Nackdong"
                      /db_xref="taxon:39947"
                      /clone="HDA1--01-C09"
                      /tissue_type="callus"
                      /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                      /lab_host="E.coli SOLR"
                      /clone_lib="OsHDAC1-overexpressing transgenic rice lambda
                      phage cDNA library I (HDA1)"
                      /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
                      XhoI; Callus was treated with ABA(20um) for 1hour. cDNA
                      was inserted into lambda Uni-ZAP XR vector at 5' end with
                      EcoRI and 3' end with XhoI site. mRNA was derived from
                      rice Histone Deacetylase overexpression line."
ORIGIN

  Query Match             40.0%;  Score 8;  DB 7;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+07;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 TGCAGGAA 14
              ||||||||
Db          4 TGCAGGAA 11


RESULT 40
AZ366451
LOCUS       AZ366451                  20 bp    DNA     linear   GSS 02-OCT-2000
DEFINITION  1M0115N07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0115N07 R, genomic survey sequence.
ACCESSION   AZ366451
VERSION     AZ366451.1  GI:10480151
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0115  row: N  column: 07
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0115N07"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
ORIGIN

  Query Match             40.0%;  Score 8;  DB 8;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+07;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 AGGAAGCG 17
              ||||||||
Db          6 AGGAAGCG 13


Search completed: August  6, 2005, 16:28:28
Job time : 1629 secs
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